

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 24, 2005, 18:43:30 ; Search time 165 Seconds
(without alignments)
21.096 Million cell updates/sec

Title: US-09-914-205-5

Perfect score: 45

Sequence: 1 FVSLKIVPI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	3 AAY95885	Human MHC
2	39	86.7	168	3 AAY99911	Peptide e
3	39	86.7	425	3 AAY99915	Peptide e
4	39	86.7	425	3 AAY99914	Peptide e
5	39	86.7	425	3 AAY99913	Peptide e
6	39	86.7	425	3 AAY99916	Peptide e
7	39	86.7	476	3 AAY99927	Peptide e
8	39	86.7	638	3 AAY99924	Peptide e
9	39	86.7	657	3 AAY95882	Peptide e
10	39	86.7	689	3 AAY99925	Peptide e
11	39	86.7	822	3 AAY99926	Peptide e
12	38	84.4	498	2 AAW37055	HIV-1 bre
13	38	84.4	498	2 AAW37054	HIV-1 bre
14	38	84.4	498	8 ADK19345	HIV DNA g
15	38	84.4	498	8 ADK19343	HIV DNA g
16	38	84.4	501	7 AAE39544	HIV gp120
17	38	84.4	501	7 AAE39543	HIV gp120
18	36	80.0	131	3 AAG01247	Human sec
19	36	80.0	169	3 AAB53585	Human col
20	36	80.0	210	3 AAB56776	Human pro
21	36	80.0	417	8 ABM84029	Human dia
22	36	80.0	453	2 AAW54356	Ubiquinol
23	36	80.0	453	6 ABM04804	Human mit
24	36	80.0	453	7 ADE61366	Human pro
25	36	80.0	453	7 ADJ70409	Human hea

26	36	80.0	453	7 ADJ68715	Human hea
27	36	80.0	453	7 ADJ70408	Human hea
28	36	80.0	453	8 ABM81716	Tumour-as
29	36	80.0	468	4 AAU33278	Novel hum
30	36	80.0	469	2 AAW37061	HIV-1 bre
31	36	80.0	469	7 AAE39552	HIV gp120
32	36	80.0	469	8 ADK19359	HIV DNA g
33	35	77.8	15	2 AAW99862	HIV-1 gpl
34	35	77.8	34	2 AAW99851	HIV-1 gpl
35	35	77.8	51	3 AAB10710	HIV-1 gpl
36	35	77.8	78	5 ABP52850	HIV-1 gpl
37	35	77.8	96	2 AAW99852	HIV-1 gpl
38	35	77.8	245	6 ABP78185	N. gonorr
39	35	77.8	245	6 ABU37576	Protein e
40	35	77.8	245	8 ADF08243	Neisseria
41	35	77.8	278	5 ABB89469	Human pol
42	35	77.8	365	2 AAW99874	Case-A2 V
43	35	77.8	453	4 AAM38830	Human pol
44	35	77.8	473	4 AAE01350	Human tum
45	35	77.8	473	4 AAM38829	Human pol

ALIGNMENTS

RESULT 1

AAY95885
ID AAY95885 standard; peptide; 9 AA.

XX AAY95885;

XX 12-SEP-2003 (revised)

DT 20-NOV-2000 (first entry)

XX Human MHC class I allele HLA-A0201 binding motif CLP-504.

XX Major histocompatibility complex class 1; MHC class 1; human; HLA-A0201;
KW HIV-1; human immunodeficiency virus type 1; gp140; immunogen;
KW DNA vaccine.

XX Human immunodeficiency virus 1.

XX WO2000050604-A1.

XX 31-AUG-2000.

XX 24-FEB-2000; 2000WO-CA000190.

XX 24-FEB-1999; 99US-00256194.

XX (CONN-) CONNAUGHT LAB LTD.

XX Sia CDY, Cao S, Persson R, Rovinski B, Parrington M;

XX WPI; 2000-565457/52.

XX Vectors comprising sequences encoding the extracellular fragment of gp140
of a primary human immunodeficiency virus (HIV)-1 isolate, useful for
vaccinating against HIV-1.

XX Claim 18; Page 18; 37pp; English.

XX The present sequence is that of CLP-504, a major histocompatibility
complex (MHC) class-I restricted motif of the extracellular envelope
fragment, gp140 (see AAY95882), of HIV-1 isolate BX08. The invention
provides vectors comprising sequences encoding gp140, useful for
vaccinating against HIV-1. The gp140 protein is rich in motifs restricted
to both the human and murine MHC class I alleles (see AAY95883-94). The
present peptide is HLA-A0201 restricted. Immunisation with an immunogen
expressing the gp140 protein leads to the generation of peptides with
class I binding capability to allow the induction of HIV-1-specific
cytotoxic T lymphocytes capable of killing virus-infected cells to limit
infection. (Updated on 12-SEP-2003 to standardise OS field)

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XX SQ - Sequence 9 AA;
Query Match 100.0%; Score 45; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
DB 1 FVSLKIVPI 9

RESULT 2
AAY99911
ID AAY99911 standard; protein; 168 AA.
XX
AC AAY99911;
XX
DT 16-NOV-2000 (first entry)
XX
DE Peptide encoded by Piece 1 DNA used in HIV DNA vaccine.
XX
KW HIV; human immunodeficiency virus; vaccine; snut;
XX silent nucleotide substitution; AIDS.
XX
OS Human immunodeficiency virus 1.
XX Synthetic.
XX
FN WO200029561-A2.
XX
PD 25-MAY-2000.
XX
PF 27-MAR-2000; 2000WO-DK000144.
XX
PR 29-MAR-1999; 99DK-00000427.
XX 09-APR-1999; 99US-0128558P.
XX (STAT-) STATENS SERUM INST.
XX
PI Fomsgaard A;
XX
DR WPI; 2000-387778/33.
XX N-PSDB; AAA49084.
XX
PT Producing nucleotide sequence construct with optimized codons for human
PT immunodeficiency virus (HIV) genetic vaccine involves obtaining a first
PT nucleotide sequence from a HIV patient, redesigning and assembling it
PT with snuts.
XX
PS Example 4; 108-109; 150pp; English.
XX
CC The present invention relates to a nucleotide construct with optimised
CC codons for use as a human immunodeficiency virus (HIV) DNA vaccine. The
CC construct uses codons from highly expressed mammalian proteins to code
CC for each derivative of an early, primary HIV envelope gene. The first
CC stage in the production of the construct was the cloning of an HIV
CC envelope gene. A nucleotide sequence encoding this gene was then created
CC using codons from highly expressed mammalian genes. The present sequence
CC is the protein encoded by one of the pieces (AAA49080-A49092) that were
CC made by assembly of snuts. Each derivative of the envelope gene (AAA49093
CC -A49097) was then built using the pieces. The HIV DNA vaccine may be used
CC as a prophylactic vaccine and as a therapeutic vaccine in HIV infected
CC patients
XX
SQ Sequence 168 AA;
Query Match 86.7%; Score 39; DB 3; Length 168;
Best Local Similarity 88.9%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 FVSLKIVPI 9
DB 145 FVSLDIVPI 153

RESULT 3
AAY99915
ID AAY99915 standard; protein; 425 AA.
XX
AC AAY99915;
XX
DT 16-NOV-2000 (first entry)
XX
DE Peptide encoded by Piece 3GVIV2 DNA used in HIV DNA vaccine.
XX
KW HIV; human immunodeficiency virus; vaccine; snut;
XX silent nucleotide substitution; AIDS.
XX
OS Human immunodeficiency virus 1.
XX Synthetic.
XX
FN WO200029561-A2.
XX
PD 25-MAY-2000.
XX
PF 27-MAR-2000; 2000WO-DK000144.
XX
PR 29-MAR-1999; 99DK-00000427.
XX 09-APR-1999; 99US-0128558P.
XX (STAT-) STATENS SERUM INST.
XX
PI Fomsgaard A;
XX
DR WPI; 2000-387778/33.
XX N-PSDB; AAA49084.
XX
PT Producing nucleotide sequence construct with optimized codons for human
PT immunodeficiency virus (HIV) genetic vaccine involves obtaining a first
PT nucleotide sequence from a HIV patient, redesigning and assembling it
PT with snuts.
XX
PS Example 4; 117-118; 150pp; English.
XX
CC The present invention relates to a nucleotide construct with optimised
CC codons for use as a human immunodeficiency virus (HIV) DNA vaccine. The
CC construct uses codons from highly expressed mammalian proteins to code
CC for each derivative of an early, primary HIV envelope gene. The first
CC stage in the production of the construct was the cloning of an HIV
CC envelope gene. A nucleotide sequence encoding this gene was then created
CC using codons from highly expressed mammalian genes. The present sequence
CC is the protein encoded by one of the pieces (AAA49080-A49092) that were
CC made by assembly of snuts. Each derivative of the envelope gene (AAA49093
CC -A49097) was then built using the pieces. The HIV DNA vaccine may be used
CC as a prophylactic vaccine and as a therapeutic vaccine in HIV infected
CC patients
XX
SQ Sequence 425 AA;
Query Match 86.7%; Score 39; DB 3; Length 425;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
DB 145 FVSLDIVPI 153

RESULT 4
AAY99914
ID AAY99914 standard; protein; 425 AA.
XX
AC AAY99914;
XX
DT 16-NOV-2000 (first entry)
XX

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DE Peptide encoded by Piece 3GV1 DNA used in HIV DNA vaccine.
XX HIV; human immunodeficiency virus; vaccine; snut;
KW silent nucleotide substitution; AIDS.
XX
XX Human immunodeficiency virus 1.
OS Synthetic.
XX
XX WO200029561-A2.
XX
XX 25-MAY-2000.
XX
XX 27-MAR-2000; 2000WO-DK000144.
XX
XX 29-MAR-1999; 99DK-00000427.
PR 09-APR-1999; 99US-0128558P.
XX
XX (STAT-) STATENS SERUM INST.
XX
XX Fomegaard A;
XX
XX WPI; 2000-387778/33.
DR N-PSDB; AAA49082.
XX
XX Producing nucleotide sequence construct with optimized codons for human
PT immunodeficiency virus (HIV) genetic vaccine involves obtaining a first
PT nucleotide sequence from a HIV patient, redesigning and assembling it
PT with snuts.
XX
XX Example 4; 112-113; 150pp; English.
XX
XX The present invention relates to a nucleotide construct with optimised
CC codons for use as a human immunodeficiency virus (HIV) DNA vaccine. The
CC construct uses codons from highly expressed mammalian proteins to code
CC for each derivative of an early, primary HIV envelope gene. The first
CC stage in the production of the construct was the cloning of an HIV
CC envelope gene. A nucleotide sequence encoding this gene was then created
CC using codons from highly expressed mammalian genes. The present sequence
CC is the protein encoded by one of the pieces (AAA49080-A49092) that were
CC made by assembly of snuts. Each derivative of the envelope gene (AAA49093
CC -A49097) was then built using the pieces. The HIV DNA vaccine may be used
CC as a prophylactic vaccine and as a therapeutic vaccine in HIV infected
CC patients
XX
XX Sequence 425 AA;
SQ
Query Match 86.7%; Score 39; DB 3; Length 425;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 FYSLKIVPI 9
Db 145 FYSLDIVPI 153

RESULT 5
AAV99913
ID AAV99913 standard; protein; 425 AA.
XX
XX AAV99913;
AC
XX
XX 16-NOV-2000 (first entry)
DT
XX
XX Peptide encoded by Piece 3 DNA used in HIV DNA vaccine.
DE
XX HIV; human immunodeficiency virus; vaccine; snut;
KW silent nucleotide substitution; AIDS.
XX
XX Human immunodeficiency virus 1.
OS Synthetic.
XX
XX WO200029561-A2.
XX
XX 25-MAY-2000.
XX
XX 27-MAR-2000; 2000WO-DK000144.
XX
XX 29-MAR-1999; 99DK-00000427.
PR 09-APR-1999; 99US-0128558P.
XX
XX (STAT-) STATENS SERUM INST.
XX
XX Fomegaard A;
XX
XX WPI; 2000-387778/33.
DR N-PSDB; AAA49083.
XX
XX Producing nucleotide sequence construct with optimized codons for human
PT immunodeficiency virus (HIV) genetic vaccine involves obtaining a first
PT nucleotide sequence from a HIV patient, redesigning and assembling it
PT with snuts.
XX
XX Example 4; 115-116; 150pp; English.
XX
XX The present invention relates to a nucleotide construct with optimised
CC codons for use as a human immunodeficiency virus (HIV) DNA vaccine. The
CC construct uses codons from highly expressed mammalian proteins to code
CC for each derivative of an early, primary HIV envelope gene. The first
CC stage in the production of the construct was the cloning of an HIV
CC envelope gene. A nucleotide sequence encoding this gene was then created
CC using codons from highly expressed mammalian genes. The present sequence
CC is the protein encoded by one of the pieces (AAA49080-A49092) that were
CC made by assembly of snuts. Each derivative of the envelope gene (AAA49093
CC -A49097) was then built using the pieces. The HIV DNA vaccine may be used
CC as a prophylactic vaccine and as a therapeutic vaccine in HIV infected
CC patients
XX
XX Sequence 425 AA;
SQ
Query Match 86.7%; Score 39; DB 3; Length 425;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 FYSLKIVPI 9
Db 145 FYSLDIVPI 153

RESULT 6
AAV99916
ID AAV99916 standard; protein; 425 AA.
XX
XX AAV99916;
AC
XX
XX 16-NOV-2000 (first entry)
DT
XX
XX Peptide encoded by Piece 3GV2 DNA used in HIV DNA vaccine.
DE
XX HIV; human immunodeficiency virus; vaccine; snut;
KW silent nucleotide substitution; AIDS.
XX
XX Human immunodeficiency virus 1.
OS Synthetic.
XX
XX WO200029561-A2.
XX
XX 25-MAY-2000.
XX
XX 27-MAR-2000; 2000WO-DK000144.
XX
XX 29-MAR-1999; 99DK-00000427.
PR 09-APR-1999; 99US-0128558P.
XX
XX (STAT-) STATENS SERUM INST.
XX
XX Fomegaard A;
XX

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XX WPI; 2000-387778/33.
 DR N-PSDB; AAA49085.
 XX
 PT Producing nucleotide sequence construct with optimized codons for human
 PT immunodeficiency virus (HIV) genetic vaccine involves obtaining a first
 PT nucleotide sequence from a HIV patient, redesigning and assembling it
 PT with snuts.
 XX
 PS Example 4; 118-119; 150pp; English.
 CC
 CC The present invention relates to a nucleotide construct with optimised
 CC codons for use as a human immunodeficiency virus (HIV) DNA vaccine. The
 CC construct uses codons from highly expressed mammalian proteins to code
 CC for each derivative of an early, primary HIV envelope gene. The first
 CC stage in the production of the construct was the cloning of an HIV
 CC envelope gene. A nucleotide sequence encoding this gene was then created
 CC using codons from highly expressed mammalian genes. The present sequence
 CC is the protein encoded by one of the pieces (AAA49080-A49092) that were
 CC made by assembly of snuts. Each derivative of the envelope gene (AAA49093
 CC -A49097) was then built using the pieces. The HIV DNA vaccine may be used
 CC as a prophylactic vaccine and as a therapeutic vaccine in HIV infected
 CC patients
 XX
 SQ Sequence 425 AA;
 Query Match 86.7%; Score 39; DB 3; Length 425;
 Best Local Similarity 88.9%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FVSLKIVPI 9
 |||||
 DB 145 FVSLDIVPI 153
 RESULT 7
 AAY99927
 ID AAY99927 standard; protein; 476 AA.
 AC AAY99927;
 DT 16-NOV-2000 (first entry)
 XX
 DE Peptide encoded by synBX08-120 gene derivative used in HIV DNA vaccine.
 XX
 KW HIV; human immunodeficiency virus; vaccine; snut;
 KW silent nucleotide substitution; AIDS.
 XX
 OS Human immunodeficiency virus 1.
 OS Synthetic.
 XX
 PN WO200029561-A2.
 XX
 PD 25-MAY-2000.
 XX
 PF 27-MAR-2000; 2000WO-DK000144.
 XX
 PR 29-MAR-1999; 99DK-00000427.
 PR 09-APR-1999; 99US-0128558P.
 XX
 PA (STAT-) STATENS SERUM INST.
 XX
 PI Fomegaard A;
 XX
 DR WPI; 2000-387778/33.
 DR N-PSDB; AAA49096.
 XX
 PT Producing nucleotide sequence construct with optimized codons for human
 PT immunodeficiency virus (HIV) genetic vaccine involves obtaining a first
 PT nucleotide sequence from a HIV patient, redesigning and assembling it
 PT with snuts.
 XX
 PS Disclosure; 146-147; 150pp; English.

XX
 CC The present invention relates to a nucleotide construct with optimised
 CC codons for use as a human immunodeficiency virus (HIV) DNA vaccine. The
 CC construct uses codons from highly expressed mammalian proteins to code
 CC for each derivative of an early, primary HIV envelope gene. The first
 CC stage in the production of the construct was the cloning of an HIV
 CC envelope gene. A nucleotide sequence encoding this gene was then created
 CC using codons from highly expressed mammalian genes. Snuts (AAA49060-
 CC A49079) were created by redesigning the nucleotide construct so that
 CC restriction enzyme sites surrounded functional regions of the sequence.
 CC Pieces (AAA49080-A49092) were made by assembly of the snuts. Each
 CC derivative of the envelope gene (AAA49093-A49097) was then built using
 CC the pieces. The present sequence is the peptide encoded by one of the
 CC gene derivatives. The HIV DNA vaccine may be used as a prophylactic
 CC vaccine and as a therapeutic vaccine in HIV infected patients
 XX
 SQ Sequence 476 AA;
 Query Match 86.7%; Score 39; DB 3; Length 476;
 Best Local Similarity 88.9%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FVSLKIVPI 9
 |||||
 DB 145 FVSLDIVPI 153
 RESULT 8
 AAY99924
 ID AAY99924 standard; protein; 638 AA.
 AC AAY99924;
 DT 16-NOV-2000 (first entry)
 XX
 DE Peptide encoded by synBX08-140 gene derivative used in HIV DNA vaccine.
 XX
 KW HIV; human immunodeficiency virus; vaccine; snut;
 KW silent nucleotide substitution; AIDS.
 XX
 OS Human immunodeficiency virus 1.
 OS Synthetic.
 XX
 PN WO200029561-A2.
 XX
 PD 25-MAY-2000.
 XX
 PF 27-MAR-2000; 2000WO-DK000144.
 XX
 PR 29-MAR-1999; 99DK-00000427.
 PR 09-APR-1999; 99US-0128558P.
 XX
 PA (STAT-) STATENS SERUM INST.
 XX
 PI Fomegaard A;
 XX
 DR WPI; 2000-387778/33.
 DR N-PSDB; AAA49093.
 XX
 PT Producing nucleotide sequence construct with optimized codons for human
 PT immunodeficiency virus (HIV) genetic vaccine involves obtaining a first
 PT nucleotide sequence from a HIV patient, redesigning and assembling it
 PT with snuts.
 XX
 PS Disclosure; 132-134; 150pp; English.
 XX
 CC The present invention relates to a nucleotide construct with optimised
 CC codons for use as a human immunodeficiency virus (HIV) DNA vaccine. The
 CC construct uses codons from highly expressed mammalian proteins to code
 CC for each derivative of an early, primary HIV envelope gene. The first
 CC stage in the production of the construct was the cloning of an HIV
 CC envelope gene. A nucleotide sequence encoding this gene was then created
 CC using codons from highly expressed mammalian genes. Snuts (AAA49060-

CC A49079) were created by redesigning the nucleotide construct so that
 CC restriction enzyme sites surrounded functional regions of the sequence.
 CC Pieces (AAA49080-A49092) were made by assembly of the snuts. Each
 CC derivative of the envelope gene (AAA49093-A49097) was then built using
 CC the pieces. The present sequence is the peptide encoded by one of the
 CC gene derivatives. The HIV DNA vaccine may be used as a prophylactic
 CC vaccine and as a therapeutic vaccine in HIV infected patients
 XX
 SQ Sequence 638 AA;

Query Match 86.7%; Score 39; DB 3; Length 638;
 Best Local Similarity 88.9%; Pred. No. 30;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
 DB 145 FYSLDIVPI 153
 ||||| |||||

RESULT 9
 AAY95882
 ID AAY95882 standard; protein; 657 AA.
 AC AAY95882;

XX
 XX 12-SEP-2003 (revised)
 DT 20-NOV-2000 (first entry)
 DT

XX HIV-1 (BX08) extracellular envelope glycoprotein gp140.

XX HIV-1; gp140; immunogen; DNA vaccine.

XX Human immunodeficiency virus 1.

XX WO2000050604-A1.

PN 31-AUG-2000.

PD 24-FEB-2000; 2000WO-CA000190.

PF 24-FEB-1999; 99US-00256194.

PR (CONN-) CONNAUGHT LAB LTD.

XX Sia CDY, Cao S, Persson R, Rovinski B, Farrington M;

XX WPI; 2000-565457/52.

DR N-PSDB; AAA50336, AAA50337.

XX Vectors comprising sequences encoding the extracellular fragment of gp140
 of a primary human immunodeficiency virus (HIV)-1 isolate, useful for
 PT vaccinating against HIV-1.

PS Disclosure; Fig 2A-F; 37pp; English.

XX The present sequence is that of the extracellular envelope fragment gp140
 CC of HIV-1 isolate BX08. The invention relates to the design and
 CC construction of HIV DNA-based immunogens capable of eliciting cell-
 CC mediated immunity. The work focussed on HIV-1 BX08 gp140 because this
 CC protein is rich in motifs restricted to both the murine and human major
 CC histocompatibility complex class I alleles (see AAY95883-94). Vectors
 CC such as pCMV.gp140.BX08 are provided that comprise a gp140 gene (see
 CC AAA50336) under control of a promoter for expression of the gene product
 CC in a host organism, thereby eliciting a cytotoxic T-cell response. The
 CC invention also includes an immunogenic composition containing the vector
 CC and a method for generating a cytotoxic T-cell response to HIV-1 in a
 CC host by administering the immunogenic composition to the host. The
 CC immunogenic compositions may be formulated for intramuscular immunisation
 CC or gene gun delivery. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 657 AA;

Query Match 86.7%; Score 39; DB 3; Length 657;

Best Local Similarity 88.9%; Pred. No. 31;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
 DB 162 FYSLDIVPI 170
 ||||| |||||

RESULT 10

AAY99925
 ID AAY99925 standard; protein; 689 AA.

XX
 AC AAY99925;

XX 16-NOV-2000 (first entry)

XX Peptide encoded by synBX08- 150 gene derivative used in HIV DNA vaccine.

XX HIV; human immunodeficiency virus; vaccine; snut;

XX silent nucleotide substitution; AIDS.

XX Human immunodeficiency virus 1.

OS Synthetic.

PN WO200029561-A2.

XX 25-MAY-2000.

XX 27-MAR-2000; 2000WO-DK000144.

XX 29-MAR-1999; 99DK-00000427.

PR 09-APR-1999; 99US-0128558P.

XX (STAT-) STATENS SERUM INST.

PI Fomsgaard A;

XX WPI; 2000-387778/33.

DR N-PSDB; AAA49094.

XX Producing nucleotide sequence construct with optimized codons for human
 immunodeficiency virus (HIV) genetic vaccine involves obtaining a first
 PT nucleotide sequence from a HIV patient, redesigning and assembling it
 PT with snuts.

XX Disclosure; 137-138; 150pp; English.

XX The present invention relates to a nucleotide construct with optimised
 CC codons for use as a human immunodeficiency virus (HIV) DNA vaccine. The
 CC construct uses codons from highly expressed mammalian proteins to code
 CC for each derivative of an early, primary HIV envelope gene. The first
 CC stage in the production of the construct was the cloning of an HIV
 CC envelope gene. A nucleotide sequence encoding this gene was then created
 CC using codons from highly expressed mammalian genes. Snuts (AAA49060-
 CC A49079) were created by redesigning the nucleotide construct so that
 CC restriction enzyme sites surrounded functional regions of the sequence.
 CC Pieces (AAA49080-A49092) were made by assembly of the snuts. Each
 CC derivative of the envelope gene (AAA49093-A49097) was then built using
 CC the pieces. The present sequence is the peptide encoded by one of the
 CC gene derivatives. The HIV DNA vaccine may be used as a prophylactic
 CC vaccine and as a therapeutic vaccine in HIV infected patients

XX Sequence 689 AA;

Query Match 86.7%; Score 39; DB 3; Length 689;

Best Local Similarity 88.9%; Pred. No. 32;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
 DB 145 FYSLDIVPI 153
 ||||| |||||

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RESULT 11
AAW37055
ID AAW37055 standard; protein; 822 AA.
XX
AC AAW37055;
XX
DT 16-NOV-2000 (first entry)
XX
DE Peptide encoded by synBX08- 160 gene derivative used in HIV DNA vaccine.
XX
KW HIV; human immunodeficiency virus; vaccine; snut;
KW silent nucleotide substitution; AIDS.
XX
OS Synthetic.
XX
FN WO200029561-A2.
XX
XX 25-MAY-2000.
XX
XX 27-MAR-2000; 2000WO-DK000144.
XX
XX 29-MAR-1999; 99DK-00000427.
XX
XX 09-APR-1999; 99US-0128558P.
XX
PA (STAT-) STATENS SERUM INST.
XX
PI Fomgaard A;
XX
XX WPI; 2000-387778/33.
XX
XX N-PSDB; AAA49095.
XX
XX Producing nucleotide sequence construct with optimized codons for human
XX immunodeficiency virus (HIV) genetic vaccine involves obtaining a first
XX nucleotide sequence from a HIV patient, redesigning and assembling it
XX with snuts.
XX
XX Disclosure; 142-144; 150pp; English.
XX
XX The present invention relates to a nucleotide construct with optimised
XX codons for use as a human immunodeficiency virus (HIV) DNA vaccine. The
XX construct uses codons from highly expressed mammalian proteins to code
XX for each derivative of an early, primary HIV envelope gene. The first
XX stage in the production of the construct was the cloning of an HIV
XX envelope gene. A nucleotide sequence encoding this gene was then created
XX using codons from highly expressed mammalian genes. Snuts (AAA49060-
XX A49079) were created by redesigning the nucleotide construct so that
XX restriction enzyme sites surrounded functional regions of the sequence.
XX Pieces (AAA49080-A49092) were made by assembly of the snuts. Each
XX derivative of the envelope gene (AAA49093-A49097) was then built using
XX the pieces. The present sequence is the peptide encoded by one of the
XX gene derivatives. The HIV DNA vaccine may be used as a prophylactic
XX vaccine and as a therapeutic vaccine in HIV infected patients
XX
SQ Sequence 822 AA;
Query Match 86.7%; Score 39; DB 3; Length 822;
Best Local Similarity 88.9%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 FYSLKIVPI 9
DB 145 FYSLDIVPI 153

RESULT 12
AAW37055
ID AAW37055 standard; protein; 498 AA.
XX
AC AAW37055;
XX
XX 17-OCT-2003 (revised)
DT 20-JUL-1998 (first entry)

```

```

XX DE HIV-1 breakthrough isolate clone C6.5 gp120 polypeptide.
XX KW HIV-1; envelope protein; gp120; MN-rgp120; vaccine; AIDS.
XX OS Human immunodeficiency virus 1.
XX FH Key Location/Qualifiers
FT Misc-difference 67
FT /note= "encoded by ANT"
XX
XX WO9801564-A1.
XX
XX 15-JAN-1998.
XX
XX 03-JUL-1997; 97WO-US009690.
XX
XX 08-JUL-1996; 96US-0676737P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Berman PW;
XX
XX WPI; 1998-101059/09.
XX
XX N-PSDB; AAV00518.
XX
XX Human immunodeficiency virus gp120 sequences from vaccine breakthrough
XX strains - useful in providing added protection against HIV not provided
XX by original vaccine.
XX
XX Claim 1; Page 95-98; 193pp; English.
XX
XX This is the deduced sequence of a gp120 envelope polypeptide of clone
XX C6.5 of a HIV-1 breakthrough isolate obtained from an individual infected
XX with HIV-1 through high risk activity while participating in Phase I or
XX Phase 2 trials of MN-rgp120, a candidate recombinant gp120 HIV-1 vaccine.
XX Nucleotide sequences (see AAV00517-30) for gp120 polypeptides (see
XX AAW37054-67) were obtained from 2 clones of each of 7 breakthrough
XX isolates. All 7 envelope glycoproteins have sequences typical of subtype
XX (clade) B viruses. The overall homology with MN-rgp120 is 69-80%. Use of
XX the gp120 polypeptides from one or more of the breakthrough isolates,
XX usually together with MN-rgp120, can provide protection against HIV
XX strains that are sufficiently different from the vaccine strain (e.g. MN-
XX rgp120) that the vaccine does not confer protection against those
XX strains. The gp120 proteins can also be used in screening assays to
XX identify antagonists of CC-CKR chemokine receptors. Antibodies induced by
XX the polypeptides are also provided. (Updated on 17-OCT-2003 to
XX standardise OS field)
XX
XX Sequence 498 AA;
Query Match 84.4%; Score 38; DB 2; Length 498;
Best Local Similarity 77.8%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 FYSLKIVPI 9
DB 156 FYSLDWPI 164

RESULT 13
AAW37054
ID AAW37054 standard; protein; 498 AA.
XX
AC AAW37054;
XX
XX 17-OCT-2003 (revised)
DT 20-JUL-1998 (first entry)
XX
XX HIV-1 breakthrough isolate clone C6.1 gp120 polypeptide.
XX KW HIV-1; envelope protein; gp120; MN-rgp120; vaccine; AIDS.
XX

```

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OS Human immunodeficiency virus 1.
XX WO9801564-A1.
PN
XX
XX
PD 15-JAN-1998.
XX
XX 03-JUL-1997; 97WO-US009690.
XX PF
XX PR 08-JUL-1996; 96US-0676737P.
XX PR
XX PA (GETH ) GENENTECH INC.
XX PI Berman PW;
XX PI
XX WPI: 1998-101059/09.
XX DR N-PSDB; AAV00517.
XX DR
XX
XX Human immunodeficiency virus gp120 sequences from vaccine breakthrough
XX PT strains - useful in providing added protection against HIV not provided
XX PT by original vaccine.
XX PT
XX PS Claim 1; Page 91-94; 193pp; English.
XX PS
XX This is the deduced sequence of a gp120 envelope polypeptide of clone
XX CC C6.1 of a HIV-1 breakthrough isolate obtained from an individual infected
XX CC with HIV-1 through high risk activity while participating in Phase I or
XX CC Phase 2 trials of MN-rgp120, a candidate recombinant gp120 HIV-1 vaccine.
XX CC Nucleotide sequences (see AAV00517-30) for gp120 polypeptides (see
XX CC AAV37054-67) were obtained from 2 clones of each of 7 breakthrough
XX CC isolates. All 7 envelope glycoproteins have sequences typical of subtype
XX CC (clade) B viruses. The overall homology with MN-rgp120 is 69-80%. Use of
XX CC the gp120 polypeptides from one or more of the breakthrough isolates,
XX CC usually together with MN-rgp120, can provide protection against HIV
XX CC strains that are sufficiently different from the vaccine strain (e.g. MN-
XX CC rgp120) that the vaccine does not confer protection against those
XX CC strains. The gp120 proteins can also be used in screening assays to
XX CC identify antagonists of CC-CKR chemokine receptors. Antibodies induced by
XX CC the polypeptides are also provided. (Updated on 17-OCT-2003 to
XX CC standardise OS field)
XX SQ Sequence 498 AA;

Query Match 84.4%; Score 38; DB 2; Length 498;
Best Local Similarity 77.8%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 156 FYSLDVVPI 164

RESULT 14
ADK19345
ID ADK19345 standard; protein; 498 AA.
XX
XX AC ADK19345;
XX
XX DT 03-JUN-2004 (first entry)
XX
XX DE HIV DNA gp120 clone C6.5.
XX
XX KW HIV; gp120; envelope glycoprotein; AIDS; vaccine; breakthrough isolate;
XX KW gp120 MN; gp120 A244; gp120 MN-GNE6; gp120 MN-GNE8; recombinant gp120;
XX KW HIV infection.
XX
XX OS Human immunodeficiency virus 1.
XX PN
XX PN US2004052821-A1.
XX PD
XX PD 18-MAR-2004.
XX
XX PF 21-FEB-2003; 2003US-00371472.
XX
XX PR 08-JUL-1996; 96US-0069891P.
XX PR 08-JUL-1997; 97US-0089841.
XX PR 15-OCT-1999; 99US-00419362.

PR 08-JUL-1996; 96US-0069891P.
PR 08-JUL-1997; 97US-0089841.
PR 15-OCT-1999; 99US-00419362.
XX
XX PA (GETH ) GENENTECH INC.
XX PI Berman PW;
XX PI
XX WPI: 2004-247705/23.
XX DR N-PSDB; ADK19344.
XX DR
XX
XX New isolated human immunodeficiency virus envelope polypeptides and
XX PT oligonucleotides encoding the gp120 glycoproteins, useful for diagnosing,
XX PT preventing or treating human immunodeficiency virus (HIV) infection.
XX PT
XX PS Claim 6; SEQ ID NO 5; 126pp; English.
XX PS
XX The invention relates to an isolated polypeptide comprising an HIV (human
XX CC immunodeficiency virus) gp120 (envelope glycoprotein 120) amino acid
XX CC sequence and its fragment from a breakthrough isolate HIV strain isolated
XX CC from a vaccinee vaccinated with the first HIV gp120 polypeptide sequence
XX CC comprises gp120 MN, gp120 A244, gp120 MN-GNE6 or gp120 MN-GNE8
XX CC (recombinant gp120). Also included are an oligonucleotide of not more
XX CC than 5 kilobases encoding the HIV gp120 polypeptide sequence, a vaccine
XX CC comprising gp120 MN and the HIV gp120 polypeptide sequence (or fragment)
XX CC in a suitable carrier and preparing an HIV vaccine (comprising adding an
XX CC HIV gp120 polypeptide sequence or its fragments from a breakthrough
XX CC isolate from a vaccinee to the vaccine with which the vaccinee was
XX CC vaccinated). The composition and methods are useful for diagnosing,
XX CC preventing or treating HIV infection (AIDS). NOTE: The authors have mixed
XX CC up the SEQ ID numbers between the sequence listing and the
XX CC description/claims, subsequently some sequences are claimed which may not
XX CC have been intended to be claimed and some sequences which were intended
XX CC to be claimed are not claimed, other sequences cannot be identified from
XX CC the information given in the patent. The present sequence represents a
XX CC gp120 protein from a breakthrough isolate HIV strain.
XX SQ Sequence 498 AA;

Query Match 84.4%; Score 38; DB 8; Length 498;
Best Local Similarity 77.8%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 156 FYSLDVVPI 164

RESULT 15
ADK19343
ID ADK19343 standard; protein; 498 AA.
XX
XX AC ADK19343;
XX
XX DT 03-JUN-2004 (first entry)
XX
XX DE HIV DNA gp120 clone C6.1.
XX
XX KW HIV; gp120; envelope glycoprotein; AIDS; vaccine; breakthrough isolate;
XX KW gp120 MN; gp120 A244; gp120 MN-GNE6; gp120 MN-GNE8; recombinant gp120;
XX KW HIV infection.
XX
XX OS Human immunodeficiency virus 1.
XX PN
XX PN US2004052821-A1.
XX PD
XX PD 18-MAR-2004.
XX
XX PF 21-FEB-2003; 2003US-00371472.
XX
XX PR 08-JUL-1996; 96US-0069891P.
XX PR 08-JUL-1997; 97US-0089841.
XX PR 15-OCT-1999; 99US-00419362.

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```

XX (GETH ) GENENTECH INC.
XX Berman PW;
XX WPI; 2004-247705/23.
XX N-PSDB; ADK19342.
XX
XX New isolated human immunodeficiency virus envelope polypeptides and
XX oligonucleotides encoding the gp120 glycoproteins, useful for diagnosing,
XX preventing or treating human immunodeficiency virus (HIV) infection.
XX
XX Claim 1; SEQ ID NO 2; 126pp; English.
XX
XX The invention relates to an isolated polypeptide comprising an HIV (human
XX immunodeficiency virus) gp120 (envelope glycoprotein 120) amino acid
XX sequence and its fragment from a breakthrough isolate HIV strain isolated
XX from a vaccinee vaccinated with the first HIV gp120 polypeptide sequence
XX comprises gp120 MN, gp120 A244, gp120 MN-GNE6 or gp120 MN-GNE8
XX (recombinant gp120). Also included are an oligonucleotide of not more
XX than 5 kilobases encoding the HIV gp120 polypeptide sequence, a vaccine
XX comprising gp120 MN and the HIV gp120 polypeptide sequence (or fragment)
XX in a suitable carrier and preparing an HIV vaccine (comprising adding an
XX HIV gp120 polypeptide sequence or its fragments from a breakthrough
XX isolate from a vaccinee to the vaccine with which the vaccinee was
XX vaccinated). The composition and methods are useful for diagnosing,
XX preventing or treating HIV infection (AIDS). NOTE: The authors have mixed
XX up the SEQ ID numbers between the sequence listing and the
XX description/claims, subsequently some sequences are claimed which may not
XX have been intended to be claimed and some sequences which were intended
XX to be claimed are not claimed, other sequences cannot be identified from
XX the information given in the patent. The present sequence represents a
XX gp120 protein from a breakthrough isolate HIV strain.
XX
XX Sequence 498 AA;
SQ
Query Match 84.4%; Score 38; DB 8; Length 498;
Best Local Similarity 77.8%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 FVSLKIVPI 9
Db 156 FVSLDVVPI 164
|||||:||||

RESULT 16
AAE39544
ID AAE39544 standard; protein; 501 AA.
XX
XX AAE39544;
AC
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX HIV gp120 protein from C6.5 clone.
DE
XX
XX Envelope glycoprotein; gp120 protein; human immunodeficiency virus; HIV;
KW immunogenic; vaccine.
XX
XX Human immunodeficiency virus.
XX
XX Key Location/Qualifiers
FH Region 2..90 /note= "Conserved region 1"
FT Misc-difference 67 /note= "Encoded by ANT"
FT Region 91..136 /note= "variable region 1"
FT Region 137..176 /note= "variable region 2"
FT Region 177..275 /note= "Conserved region 2"
FT Region 276..310 /note= "variable region 3"
FT

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FT Region 311..356 /note= "Conserved region 3"
FT Region 363..416 /note= "Conserved region 4 and variable region 4"
FT Region 430..441 /note= "Variable region 5"
FT Region 442..484 /note= "Conserved region 5"
FT Misc-difference 499..501 /note= "These residues are absent in the sequence shown as SEQ ID NO: 5 in column 83-86 of the specification"
FT Misc-difference 499 /note= "Encoded by TAA; This residue is absent in the sequence shown in column 79-83 of the specification"
FT
XX US6585979-B1.
XX 01-JUL-2003.
PD
XX 15-OCT-1999; 99US-00419362.
XX
XX 08-JUL-1997; 97US-00889841.
XX 17-DEC-1997; 97US-0069891P.
XX (GETH ) GENENTECH INC.
XX Berman PW;
XX WPI; 2003-707284/67.
XX N-PSDB; AAD60060.
XX
XX An immunogenic composition, useful as a vaccine against HIV, comprises a
XX polypeptide having a gp120 MN sequence and a polypeptide having a
XX breakthrough isolate gp120, in a carrier.
XX
XX Claim 1; Col 9-13; 117pp; English.
XX
XX The present invention relates to envelope glycoproteins (gp120) proteins
XX from breakthrough isolates of human immunodeficiency virus (HIV) trials.
XX The invention also relates to an immunogenic composition comprising a
XX gp120 MN sequence and a polypeptide having a breakthrough isolate gp120,
XX in a carrier. The composition is useful as a vaccine against HIV. The
XX present sequence is HIV gp120 protein
XX
XX Sequence 501 AA;
SQ
Query Match 84.4%; Score 38; DB 7; Length 501;
Best Local Similarity 77.8%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 FVSLKIVPI 9
Db 156 FVSLDVVPI 164
|||||:||||

RESULT 17
AAE39543
ID AAE39543 standard; protein; 501 AA.
XX
XX AAE39543;
AC
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX HIV gp120 protein from C6.1 clone.
DE
XX
XX Envelope glycoprotein; gp120 protein; human immunodeficiency virus; HIV;
KW immunogenic; vaccine.
XX
XX Human immunodeficiency virus.
XX
XX Key Location/Qualifiers
FH Region 2..90 /note= "Conserved region 1"
FT

```


FT Region 91. .136
 FT /note= "Variable region 1"
 FT Region 137. .176
 FT /note= "Variable region 2"
 FT Region 177. .275
 FT /note= "Conserved region 2"
 FT Region 276. .310
 FT /note= "Variable region 3"
 FT Region 311. .356
 FT /note= "Conserved region 3"
 FT Region 363. .416
 FT /note= "Conserved region 4 and variable region 4"
 FT Region 430. .441
 FT /note= "Variable region 5"
 FT Region 442. .484
 FT /note= "Conserved region 5"
 FT Misc-difference 499. .501
 FT /note= "These residues are absent in the sequence shown
 FT as SEQ ID NO: 2 in column 75-80 of the specification"
 FT Misc-difference 499
 FT /note= "Encoded by TAA; This residue is absent in the
 FT sequence shown in column 73-76 of the specification"
 XX
 PN US6585979-B1.
 XX
 XX 01-JUL-2003.
 XX
 PF 15-OCT-1999; 99US-00419362.
 XX
 PR 08-JUL-1997; 97US-00889841.
 PR 17-DEC-1997; 97US-0069891P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Berman PW;
 XX
 DR WPI; 2003-707284/67.
 DR N-PSDB; AAD60059.
 XX
 XX An immunogenic composition, useful as a vaccine against HIV, comprises a
 PT polypeptide having a gp120 MN sequence and a polypeptide having a
 PT breakthrough isolate gp120, in a carrier.
 XX
 PS Claim 1; Col 8-9; 117pp; English.
 XX
 CC The present invention relates to envelope glycoproteins (gp120) proteins
 CC from breakthrough isolates of human immunodeficiency virus (HIV) trials.
 CC The invention also relates to an immunogenic composition comprising a
 CC gp120 MN sequence and a polypeptide having a breakthrough isolate gp120,
 CC in a carrier. The composition is useful as a vaccine against HIV. The
 CC present sequence is HIV gp120 protein
 XX
 SQ Sequence 501 AA;
 Query Match 84.4%; Score 38; DB 7; Length 501;
 Best Local Similarity 77.8%; Pred. No. 37;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FYSLKIVPI 9
 DB 156 FYSLDVWPI 164
 RESULT 18
 AAG01247
 ID AAG01247 standard; protein; 131 AA.
 XX
 AC AAG01247;
 XX
 XX 06-OCT-2000 (first entry)
 DT
 DE Human secreted protein, SEQ ID NO: 5328.
 DE
 XX

KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-00200610.
 XX
 PR 26-FEB-1999; 99US-0122487P.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 DR WPI; 2000-500381/45.
 DR N-PSDB; AAC01253.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 PS Claim 13; SEQ ID NO 5328; 71pp + Sequence Listing; English.
 XX
 CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX
 SQ Sequence 131 AA;
 Query Match 80.0%; Score 36; DB 3; Length 131;
 Best Local Similarity 75.0%; Pred. No. 23;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FYSLKIVP 8
 DB 13 FYSLKVAP 20
 RESULT 19
 AAB53585
 ID AAB53585 standard; protein; 169 AA.
 XX
 AC AAB53585;
 XX
 DT 09-MAR-2001 (first entry)
 DE
 DE Human colon cancer antigen protein sequence SEQ ID NO:1125.
 XX
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW identification; cytostatic; cardioactive; neuroprotective; vulnery;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW nephrotropic; antineoplastic; antibacterial; gene therapy; wound;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; renal disorder;
 KW infectious disease; cardiovascular disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO2000055351-A1.
 XX

```
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005883.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587534/55.
DR N-PSDB; AAC98342.
XX
PT Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer.
XX
PS Claim 11; Page 1715; 2104pp; English.
XX
CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
CC vulnery, nephrotropic, antiinfective and antibacterial activities, and
CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridisation probes. The proteins may
CC also be used to prevent diseases such as neural disorders, immune system
CC disorders, muscular disorders, reproductive disorders, gastrointestinal
CC disorders, wounds, renal disorders, infectious diseases, and
CC cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 169 AA;
Query Match 80.0%; Score 36; DB 3; Length 169;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FVSLKIVP 8
DB 14 FVSLKVAP 21
RESULT 20
AAB56776
ID AAB56776 standard; protein; 210 AA.
XX
AC AAB56776;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen protein sequence SEQ ID NO:1354.
XX
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease.
XX
OS Homo sapiens.
XX
PN WO2000055174-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005988.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587534/55.
DR N-PSDB; AAC98342.
XX
PT Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer.
XX
PS Claim 11; Page 1715; 2104pp; English.
XX
CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
CC vulnery, nephrotropic, antiinfective and antibacterial activities, and
CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridisation probes. The proteins may
CC also be used to prevent diseases such as neural disorders, immune system
CC disorders, muscular disorders, reproductive disorders, gastrointestinal
CC disorders, wounds, renal disorders, infectious diseases, and
CC cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 169 AA;
Query Match 80.0%; Score 36; DB 3; Length 169;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FVSLKIVP 8
DB 14 FVSLKVAP 21
RESULT 21
AAB56776
ID AAB56776 standard; protein; 417 AA.
XX
AC AAB56776;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4278.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Deleane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SE, Rioux P, Shen EU, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
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XX WPI; 2004-329368/30.
 DR N-PSDB; ACN42681.
 XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX
 PS Claim 27; Page; 190pp; English.
 XX
 CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorders, developmental disorders, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX
 SQ Sequence 417 AA;
 Query Match 80.0%; Score 36; DB 8; Length 417;
 Best Local Similarity 75.0%; Pred. No. 80;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FYSLKIVP 8
 Db 13 FYSLKVP 20
 |||||:|
 RESULT 22
 AAWS4356
 ID AAWS4356 standard; protein; 453 AA.
 XX
 AC AAWS4356;
 XX
 DT 14-AUG-1998 (first entry)
 XX
 DE Ubiquinolcytochrom C reductase complex core protein 2 precursor.
 XX
 KW Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
 KW 2D gel electrophoresis; detection.
 XX
 OS Homo sapiens.
 XX
 PN WO9810291-A1.
 XX
 PD 12-MAR-1998.
 XX
 PF 05-SEP-1997; 97WO-GB002394.
 XX
 PR 06-SEP-1996; 96GB-00018600.
 PR 08-APR-1997; 97GB-00007132.
 XX
 PA (CLIN-) CENT CLINICAL & BASIC RES.
 XX
 PI Byrjalsen I, Larsen P, Fey SJ;
 XX
 DR WPI; 1998-207057/18.
 XX
 PT Biochemical markers of human endometrium - useful for, e.g. diagnosis of
 PT hyperplasia and adenocarcinoma.
 XX
 PS Disclosure; Page 21; 77pp; English.

XX Proteins AAWS4349-W54364 are examples of proteins produced in the
 CC endometrium during the hyperplasia, adenocarcinoma or proliferative phase
 CC of the endometrium. The presence and quantities of these proteins can be
 CC detected using 2D gel electrophoresis comparison of cell lysates. The
 CC proteins can be used as biochemical markers to detect the phase of the
 CC endometrium and can be measured in body fluids, obviating the need for
 CC endometrial biopsies
 XX
 SQ Sequence 453 AA;
 Query Match 80.0%; Score 36; DB 2; Length 453;
 Best Local Similarity 75.0%; Pred. No. 87;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FYSLKIVP 8
 Db 13 FYSLKVP 20
 |||||:|
 RESULT 23
 ABM04804
 ID ABM04804 standard; protein; 453 AA.
 XX
 AC ABM04804;
 XX
 DT 22-SEP-2003 (first entry)
 XX
 DE Human mitochondrial cytochrome bc-1 complex core protein II.
 XX
 KW spinal cord; neuropathic pain; central sensitisation pain; pain;
 KW analgesic; gene therapy.
 OS Homo sapiens.
 XX
 PN EP1284298-A2.
 XX
 PD 19-FEB-2003.
 XX
 PF 26-JUL-2002; 2002EP-00255229.
 XX
 PR 27-JUL-2001; 2001GB-00018354.
 PR 07-FEB-2002; 2002GB-00002883.
 XX
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Brooksbank RA, Dixon AK, Lee K, Pinnock RD;
 XX
 DR WPI; 2003-543489/52.
 DR N-PSDB; ACF25346.
 XX
 PT Use of an isolated gene sequence in the screening of compounds for
 PT diagnosing or treating pain.
 XX
 PS Claim 1; Page 85-86; 188pp; English.
 XX
 CC The invention relates to a novel isolated gene sequence that is
 CC downregulated in the spinal cord of a mammal in response to mechanically
 CC distinct first and second models of neuropathic or central sensitisation
 CC pain, useful in the screening of compounds for diagnosing or treating
 CC pain. A protein encoded by a gene of the invention has analgesic
 CC activity. A polynucleotide of the invention may have a use in gene
 CC therapy. The gene sequence is useful for preparing a composition for
 CC diagnosing or treating pain. The present sequence represents a protein
 CC encoded by a gene of the invention
 XX
 SQ Sequence 453 AA;
 Query Match 80.0%; Score 36; DB 6; Length 453;
 Best Local Similarity 75.0%; Pred. No. 87;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FYSLKIVP 8

|||||: |
13 FYSLKVP 20

Db

RESULT 24
ADE61366
ID ADE61366 standard; protein; 453 AA.
XX
AC ADE61366;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P22695, SEQ ID NO 7284.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P22695.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 453 AA;

Query Match 80.0%; Score 36; DB 7; Length 453;
Best Local Similarity 75.0%; Pred. No. 87;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 FYSLKVP 8
Db 13 FYSLKVP 20
|||: |
|||: |

RESULT 25
ADJ70409
ID ADJ70409 standard; protein; 453 AA.
XX
AC ADJ70409;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID2215.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy, ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-039987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
DR WPI; 2003-845369/78.
XX
PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 2215; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 453 AA;

Query Match 80.0%; Score 36; DB 7; Length 453;

Best Local Similarity 75.0%; Pred. No. 87;		Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
OY	1 FYSLKIVP 8	Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Db	13 FYSLKVAP 20		
RESULT 26			
ADJ68715	ADJ68715 standard; protein; 453 AA.		
XX	AC	ADJ68715;	
XX	DT	06-MAY-2004 (first entry)	
XX	DE	Human heat mitochondrial protein as a therapeutic target SeqID521.	
XX	KW	mitochondrial; human; screening assay; diabetes mellitus;	
XX	KW	Huntington's disease; osteoarthritis;	
XX	KW	Leber's hereditary optic neuropathy; LHON;	
XX	KW	mitochondrial encephalopathy lactic acidosis and stroke; MELAS;	
XX	KW	myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;	
XX	KW	neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;	
XX	KW	osteopathic; ophthalmological; cytostatic.	
XX	OS	Homo sapiens.	
XX	PN	WO2003087768-A2.	
XX	PD	23-OCT-2003.	
XX	PF	04-APR-2003; 2003WO-US010870.	
XX	PR	12-APR-2002; 2002US-0372843P.	
XX	PR	17-JUN-2002; 2002US-0389987P.	
XX	PR	20-SEP-2002; 2002US-0412418P.	
XX	PA	(MITO-) MITOKOR.	
XX	PA	(BUCK-) BUCK INST AGE RES.	
XX	PI	Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;	
XX	PI	Warnock DE;	
XX	DR	WPI; 2003-845369/78.	
XX	PT	Identifying a mitochondrial target for drug screening assays and for	
XX	PT	treating diseases associated with altered mitochondrial function,	
XX	PT	comprises detecting a modified polypeptide in a sample and correlating	
XX	PT	with the disease.	
XX	PS	Claim 1; SEQ ID NO 521; 180pp; English.	
XX	CC	This invention relates to novel mitochondrial targets that can be used	
XX	CC	for therapeutic intervention in treating a disease associated with	
XX	CC	altered mitochondrial function. Specifically, it refers to a method for	
XX	CC	identifying proteins of the human heart mitochondrial proteome that are	
XX	CC	useful for drug screening assays, as well as therapeutic targets. The	
XX	CC	present invention describes a method for identifying such proteins that	
XX	CC	can be used in the treatment of various diseases associated with altered	
XX	CC	mitochondrial function including diabetes mellitus, Huntington's disease,	
XX	CC	osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial	
XX	CC	encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy	
XX	CC	ragged red fibre syndrome (MERRF) or cancer. Accordingly, these	
XX	CC	compositions have neuroprotective, nootropic, antidiabetic,	
XX	CC	anticonvulsant, antiarthritic, osteopathic, ophthalmological and	
XX	CC	cytostatic activities. This polypeptide sequence is a human heart	
XX	CC	mitochondrial protein of the invention.	
XX	SQ	Sequence 453 AA;	
Query Match		80.0%; Score 36; DB 7; Length 453;	
Best Local Similarity		75.0%; Pred. No. 87;	
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			

Best Local Similarity 75.0%; Pred. No. 87;		Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
OY	1 FYSLKIVP 8	Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Db	13 FYSLKVAP 20		
RESULT 27			
ADJ70408	ADJ70408 standard; protein; 453 AA.		
XX	AC	ADJ70408;	
XX	DT	06-MAY-2004 (first entry)	
XX	DE	Human heat mitochondrial protein as a therapeutic target SeqID2214.	
XX	KW	mitochondrial; human; screening assay; diabetes mellitus;	
XX	KW	Huntington's disease; osteoarthritis;	
XX	KW	Leber's hereditary optic neuropathy; LHON;	
XX	KW	mitochondrial encephalopathy lactic acidosis and stroke; MELAS;	
XX	KW	myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;	
XX	KW	neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;	
XX	KW	osteopathic; ophthalmological; cytostatic.	
XX	OS	Homo sapiens.	
XX	PN	WO2003087768-A2.	
XX	PD	23-OCT-2003.	
XX	PF	04-APR-2003; 2003WO-US010870.	
XX	PR	12-APR-2002; 2002US-0372843P.	
XX	PR	17-JUN-2002; 2002US-0389987P.	
XX	PR	20-SEP-2002; 2002US-0412418P.	
XX	PA	(MITO-) MITOKOR.	
XX	PA	(BUCK-) BUCK INST AGE RES.	
XX	PI	Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;	
XX	PI	Warnock DE;	
XX	DR	WPI; 2003-845369/78.	
XX	PT	Identifying a mitochondrial target for drug screening assays and for	
XX	PT	treating diseases associated with altered mitochondrial function,	
XX	PT	comprises detecting a modified polypeptide in a sample and correlating	
XX	PT	with the disease.	
XX	PS	Claim 1; SEQ ID NO 2214; 180pp; English.	
XX	CC	This invention relates to novel mitochondrial targets that can be used	
XX	CC	for therapeutic intervention in treating a disease associated with	
XX	CC	altered mitochondrial function. Specifically, it refers to a method for	
XX	CC	identifying proteins of the human heart mitochondrial proteome that are	
XX	CC	useful for drug screening assays, as well as therapeutic targets. The	
XX	CC	present invention describes a method for identifying such proteins that	
XX	CC	can be used in the treatment of various diseases associated with altered	
XX	CC	mitochondrial function including diabetes mellitus, Huntington's disease,	
XX	CC	osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial	
XX	CC	encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy	
XX	CC	ragged red fibre syndrome (MERRF) or cancer. Accordingly, these	
XX	CC	compositions have neuroprotective, nootropic, antidiabetic,	
XX	CC	anticonvulsant, antiarthritic, osteopathic, ophthalmological and	
XX	CC	cytostatic activities. This polypeptide sequence is a human heart	
XX	CC	mitochondrial protein of the invention.	
XX	SQ	Sequence 453 AA;	
Query Match		80.0%; Score 36; DB 7; Length 453;	
Best Local Similarity		75.0%; Pred. No. 87;	
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			

QY	1 FYSLKIVP 8 :	13 FYSLKVP 20	Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
DB							
RESULT 28							
ARM81716							
ID	ABM81716 standard; protein; 453 AA.						
XX	AC						
XX	ABM81716;						
DT	18-NOV-2004 (first entry)						
XX							
DE	Tumour-associated antigenic target (TAT) polypeptide PRO3640, SEQ:4422.						
XX							
KW	Tumour-associated antigenic target; TAT; human; overexpression; cancer;						
KW	tumour; diagnosis; cell proliferative disorder; breast cancer;						
KW	colorectal cancer; lung cancer; ovarian cancer; liver cancer;						
KW	central nervous system cancer; bladder cancer; pancreatic cancer;						
KW	cervical cancer; melanoma; leukaemia; hybridisation probe;						
KW	chromosome identification; chromosome mapping; gene mapping;						
KW	gene therapy; cytostatic.						
XX							
OS	Homo sapiens.						
XX							
PN	WO2004030615-A2.						
XX							
PD	15-APR-2004.						
XX							
PF	29-SEP-2003; 2003WO-US028547.						
XX							
PR	02-OCT-2002; 2002US-0414971P.						
XX							
PA	(GETH) GENENTECH INC.						
XX							
PI	Wu TD, Zhang Z, Zhou Y;						
XX							
DR	WPI; 2004-347921/32.						
XX							
DR	N-PSDB; ACN39949.						
XX							
PT	New tumor-associated antigenic target polypeptides and nucleic acids,						
XX	useful in preparing a medicament for treating or detecting a						
PT	proliferative disorder, e.g. breast, lung, colorectal, ovarian or						
XX	prostate cancer or tumor.						
PS	Claim 12; SEQ ID NO 4422; 7273pp; English.						
XX							
CC	The invention relates to human tumour-associated antigenic target (TAT)						
CC	polypeptides, and their related nucleic acids. The TAT polypeptides are						
CC	overexpressed in cancer tissues compared to normal tissues, and may thus						
CC	serve as effective targets for the diagnosis and treatment of cancer in						
CC	mammals. The invention also relates to nucleic acid and polypeptide						
CC	sequences at least 80% identical to the TAT nucleic acids and						
CC	polypeptides; expression vectors and host cells comprising a TAT nucleic						
CC	acid; an antibody specific for a TAT polypeptide; a peptide or organic						
CC	molecule which binds to a TAT polypeptide; fusion proteins comprising a						
CC	TAT polypeptide; and methods and compositions for the treatment or						
CC	diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,						
CC	antibodies, antagonists, binding molecules and compositions are useful						
CC	for diagnosing or treating a cell proliferative disorder associated with						
CC	increased TAT expression, particularly cancers such as breast cancer,						
CC	colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder						
CC	cancer, pancreatic cancer, cervical cancer, cancers of the central						
CC	nervous system, melanoma and leukaemia. TAT nucleic acids may further be						
CC	used as hybridisation probes, in chromosome and gene mapping, in						
CC	chromosome identification and in gene therapy. The present sequence						
CC	represents a TAT polypeptide of the invention						
XX							
SQ	Sequence 453 AA;						
	Query Match	80.0%;	Score 36;	DB 8;	Length 453;		
	Best Local Similarity	75.0%;	Pred. No. 87;				
	Matches	6; Conservative	1; Mismatches	1			

QY	1 FYSLKIVP 8 :	13 FYSLKVP 20	Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
DB							
RESULT 29							
AAU33278							
ID	AAU33278 standard; protein; 468 AA.						
XX	AC						
XX	AAU33278;						
DT	18-DEC-2001 (first entry)						
XX							
DE	Novel human secreted protein #3769.						
XX							
KW	Human; vaccination; gene therapy; nutritional supplement;						
KW	stem cell proliferation; haematopoiesis; nerve tissue regeneration;						
KW	immune suppression; immune stimulation; anti-inflammatory; leukaemia.						
XX							
OS	Homo sapiens.						
XX							
PN	WO200179449-A2.						
XX							
PD	25-OCT-2001.						
XX							
PF	16-APR-2001; 2001WO-US008656.						
XX							
PR	18-APR-2000; 2000US-00552929.						
XX							
PR	26-JAN-2001; 2001US-00770160.						
XX							
PA	(HYSE-) HYSEQ INC.						
XX							
PI	Tang YT, Liu C, Drmanac RT;						
XX							
DR	WPI; 2001-611725/70.						
XX							
PT	Nucleic acids encoding a range of human polypeptides, useful in genetic						
XX	vaccination, testing and therapy.						
PS	Claim 20; Page 753; 765pp; English.						
XX							
CC	The invention relates to novel human secreted polypeptides. The						
CC	polypeptides and antibodies to the polypeptides are useful for						
CC	determining the presence of or predisposition to a disease associated						
CC	with altered levels of polypeptide. The polypeptides are also useful for						
CC	identifying agents (agonists and antagonists) that bind to them. Cells						
CC	expressing the proteins are useful for identifying a therapeutic agent						
CC	for use in treatment of a pathology related to aberrant expression or						
CC	physiological interactions of the polypeptide. Vectors comprising the						
CC	nucleic acids encoding the polypeptides and cells genetically engineered						
CC	to express them are also useful for producing the proteins. The proteins						
CC	are useful in genetic vaccination, testing and therapy, and can be used						
CC	as nutritional supplements. They may be used to increase stem cell						
CC	proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon						
CC	and/or nerve tissue growth or regeneration; immune suppression and/or						
CC	stimulation; as anti-inflammatory agents; and in treatment of leukaemias.						
CC	AAU29510-AAU3304 represent the amino acid sequences of novel human						
XX	secreted proteins of the invention						
SQ	Sequence 468 AA;						
	Query Match	80.0%;	Score 36;	DB 4;	Length 468;		
	Best Local Similarity	75.0%;	Pred. No. 90;				
	Matches	6; Conservative	1; Mismatches	1			

QY	1 FYSLKIVP 8 :	13 FYSLKVP 20	Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
DB							
RESULT 30							
AAU33278							
ID	AAU33278 standard; protein; 468 AA.						
XX	AC						
XX	AAU33278;						
DT	18-DEC-2001 (first entry)						
XX							
DE	Novel human secreted protein #3769.						
XX							
KW	Human; vaccination; gene therapy; nutritional supplement;						
KW	stem cell proliferation; haematopoiesis; nerve tissue regeneration;						
KW	immune suppression; immune stimulation; anti-inflammatory; leukaemia.						
XX							
OS	Homo sapiens.						
XX							
PN	WO200179449-A2.						
XX							
PD	25-OCT-2001.						
XX							
PF	16-APR-2001; 2001WO-US008656.						
XX							
PR	18-APR-2000; 2000US-00552929.						
XX							
PR	26-JAN-2001; 2001US-00770160.						
XX							
PA	(HYSE-) HYSEQ INC.						
XX							
PI	Tang YT, Liu C, Drmanac RT;						
XX							
DR	WPI; 2001-611725/70.						
XX							
PT	Nucleic acids encoding a range of human polypeptides, useful in genetic						
XX	vaccination, testing and therapy.						
PS	Claim 20; Page 753; 765pp; English.						
XX							
CC	The invention relates to novel human secreted polypeptides. The						
CC	polypeptides and antibodies to the polypeptides are useful for						
CC	determining the presence of or predisposition to a disease associated						
CC	with altered levels of polypeptide. The polypeptides are also useful for						
CC	identifying agents (agonists and antagonists) that bind to them. Cells						
CC	expressing the proteins are useful for identifying a therapeutic agent						
CC	for use in treatment of a pathology related to aberrant expression or						
CC	physiological interactions of the polypeptide. Vectors comprising the						
CC	nucleic acids encoding the polypeptides and cells genetically engineered						
CC	to express them are also useful for producing the proteins. The proteins						
CC	are useful in genetic vaccination, testing and therapy, and can be used						
CC	as nutritional supplements. They may be used to increase stem cell						
CC	proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon						
CC	and/or nerve tissue growth or regeneration; immune suppression and/or						
CC	stimulation; as anti-inflammatory agents; and in treatment of leukaemias.						
CC	AAU29510-AAU3304 represent the amino acid sequences of novel human						
XX	secreted proteins of the invention						
SQ	Sequence 468 AA;						
	Query Match	80.0%;	Score 36;	DB 4;	Length 468;		
	Best Local Similarity	75.0%;	Pred. No. 90;				
	Matches	6; Conservative	1; Mismatches	1			

QY	1 FYSLKIVP 8 :	13 FYSLKVP 20	Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
DB							
RESULT 30							
AAU33278							
ID	AAU33278 standard; protein; 468 AA.						
XX	AC						
XX	AAU33278;						
DT	18-DEC-2001 (first entry)						
XX							
DE	Novel human secreted protein #3769.						
XX							
KW	Human; vaccination; gene therapy; nutritional supplement;						
KW	stem cell proliferation; haematopoiesis; nerve tissue regeneration;						
KW	immune suppression; immune stimulation; anti-inflammatory; leukaemia.						
XX							
OS	Homo sapiens.						
XX							
PN	WO200179449-A2.						
XX							
PD	25-OCT-2001.						
XX							
PF	16-APR-2001; 2001WO-US008656.						
XX							
PR	18-APR-2000; 2000US-00552929.						
XX							
PR	26-JAN-2001; 2001US-00770160.						
XX							
PA	(HYSE-) HYSEQ INC.						
XX							
PI	Tang YT, Liu C, Drmanac RT;						
XX							
DR	WPI; 2001-611725/70.						
XX							
PT	Nucleic acids encoding a range of human polypeptides, useful in genetic						
XX	vaccination, testing and therapy.						
PS	Claim 20; Page 753; 765pp; English.						
XX							
CC	The invention relates to novel human secreted polypeptides. The						
CC	polypeptides and antibodies to the polypeptides are useful for						
CC	determining the presence of or predisposition to a disease associated						
CC	with altered levels of polypeptide. The polypeptides are also useful for						
CC	identifying agents (agonists and antagonists) that bind to them. Cells						
CC	expressing the proteins are useful for identifying a therapeutic agent						
CC	for use in treatment of a pathology related to aberrant expression or						
CC	physiological interactions of the polypeptide. Vectors comprising the						
CC	nucleic acids encoding the polypeptides and cells genetically engineered						
CC	to express them are also useful for producing the proteins. The proteins						
CC	are useful in genetic vaccination, testing and therapy, and can be used						
CC	as nutritional supplements. They may be used to increase stem cell						
CC	proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon						
CC	and/or nerve tissue growth or regeneration; immune suppression and/or						
CC	stimulation; as anti-inflammatory agents; and in treatment of leukaemias.						
CC	AAU29510-AAU3304 represent the amino acid sequences of novel human						
XX	secreted proteins of the invention						
SQ	Sequence 468 AA;						
	Query Match	80.0%;	Score 36;	DB 4;	Length 468;		
	Best Local Similarity	75.0%;	Pred. No. 90;				
	Matches	6; Conservative	1; Mismatches	1			

QY	1 FYSLKIVP 8 :	13 FYSLKVP 20	Matches	6; Conservative	1; Mismatches	1; Indels	0; Gaps
DB							
RESULT 30							
AAU33278							
ID	AAU33278 standard; protein; 468 AA.						
XX	AC						
XX	AAU33278;						
DT	18-DEC-2001 (first entry)						
XX							
DE	Novel human secreted protein #3769.						

AAW37061
ID AAW37061 standard; protein; 469 AA.
XX AC AAW37061;
XX
DT 17-OCT-2003 (revised)
DT 20-JUL-1998 (first entry)
XX
DE HIV-1 breakthrough isolate clone C7.10 gp120 polypeptide.
XX
KW HIV-1; envelope protein; gp120; MN-rgp120; vaccine; AIDS.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9801564-A1.
XX
PD 15-JAN-1998.
XX
PF 03-JUL-1997; 97WO-US009690.
XX
PR 08-JUL-1996; 96US-0676737P.
XX
PA (GETH) GENENTECH INC.
XX Berman PW;
XX
DR WPI; 1998-101059/09.
DR N-PSDB; AAW00524.
XX
PT Human immunodeficiency virus gp120 sequences from vaccine breakthrough strains - useful in providing added protection against HIV not provided by original vaccine.
PS Claim 1; Page 121-123; 193pp; English.
XX
CC This is the deduced sequence of a gp120 envelope polypeptide of clone C7.10 of a HIV-1 breakthrough isolate obtained from an individual infected with HIV-1 through high risk activity while participating in Phase 1 or Phase 2 trials of MN-rgp120, a candidate recombinant gp120 HIV -1 vaccine. Nucleotide sequences (see AAW00517-30) for gp120 polypeptides (see AAW37054-67) were obtained from 2 clones of each of 7 breakthrough isolates. All 7 envelope glycoproteins have sequences typical of subtype (clade) B viruses. The overall homology with MN-rgp120 is 69-80%. Use of the gp120 polypeptides from one or more of the breakthrough isolates, usually together with MN-rgp120, can provide protection against HIV strains that are sufficiently different from the vaccine strain (e.g. MN-rgp120) that the vaccine does not confer protection against those strains. The gp120 proteins can also be used in screening assays to identify antagonists of CC-CKR chemokine receptors. Antibodies induced by CC the polypeptides are also provided. (Updated on 17-OCT-2003 to CC standardise OS field)
XX
SQ Sequence 469 AA;
Query Match 80.0%; Score 36; DB 2; Length 469;
Best Local Similarity 77.8%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 FYSLKIVPI 9
DB 140 FYKLNIIVPI 148
RESULT 31
AAE39552
ID AAE39552 standard; protein; 469 AA.
XX
AC AAE39552;
XX
DT 18-DEC-2003 (first entry)
XX
DE HIV gp120 protein from C7.10 clone.
XX

KW Envelope glycoprotein; gp120 protein; human immunodeficiency virus; HIV; immunogenic; vaccine.
XX
OS Human immunodeficiency virus.
XX
FH Key
FT Region 1. .89
FT Region /note= "Conserved region 1"
FT Region 90. .120
FT Region /note= "Variable region 1"
FT Region 121. .158
FT Region /note= "Variable region 2"
FT Region 159. .257
FT Region /note= "Conserved region 2"
FT Region 258. .292
FT Region /note= "Variable region 3"
FT Region 293. .337
FT Region /note= "Conserved region 3"
FT Region 346. .403
FT Region /note= "Conserved region 4 and variable region 4"
FT Region 417. .432
FT Region /note= "Variable region 5"
FT Region 433. .469
FT Region /note= "Conserved region 5"
XX
PN US5585979-B1.
XX
XX
PD 01-JUL-2003.
XX
XX 15-OCT-1999; 99US-00419362.
PF
XX 08-JUL-1997; 97US-00899841.
PR
PR 17-DEC-1997; 97US-0069891P.
XX
XX (GETH) GENENTECH INC.
XX
XX Berman PW;
XX
DR WPI; 2003-707284/67.
DR N-PSDB; AAD60066.
XX
PT An immunogenic composition, useful as a vaccine against HIV, comprises a polypeptide having a gp120 MN sequence and a polypeptide having a breakthrough isolate gp120, in a carrier.
XX
PS Claim 1; Col 27-31; 117pp; English.
XX
CC The present invention relates to envelope glycoproteins (gp120) proteins from breakthrough isolates of human immunodeficiency virus (HIV) trials. The invention also relates to an immunogenic composition comprising a gp120 MN sequence and a polypeptide having a breakthrough isolate gp120, in a carrier. The composition is useful as a vaccine against HIV. The present sequence is HIV gp120 protein
XX
SQ Sequence 469 AA;
Query Match 80.0%; Score 36; DB 7; Length 469;
Best Local Similarity 77.8%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 FYSLKIVPI 9
DB 140 FYKLNIIVPI 148
RESULT 32
ADK19359
ID ADK19359 standard; protein; 469 AA.
XX
AC ADK19359;
XX
DT 03-JUN-2004 (first entry)
XX

DE HIV DNA gp120 clone C7.10.
 XX
 KW HIV; gp120; envelope glycoprotein; AIDS; vaccine; breakthrough isolate;
 KW gp120 MN; gp120 A244; gp120 MN-GNE6; gp120 MN-GNE8; recombinant gp120;
 KW HIV infection.
 XX
 OS Human immunodeficiency virus 1.
 XX
 FN US2004052821-A1.
 FN
 PD 18-MAR-2004.
 XX
 PF 21-FEB-2003; 2003US-00371472.
 XX
 XX 08-JUL-1996; 96US-0069891P.
 PR 08-JUL-1997; 97US-00889841.
 PR 15-OCT-1999; 99US-00419362.
 XX
 PA (GETH) GENENTECH INC.
 XX
 FI Berman PW;
 XX
 DR WPI; 2004-247705/23.
 DR N-P8DB; ADK19358.
 XX
 PT New isolated human immunodeficiency virus envelope polypeptides and
 PT oligonucleotides encoding the gp120 glycoproteins, useful for diagnosing,
 PT preventing or treating human immunodeficiency virus (HIV) infection.
 XX
 PS Claim 6; SEQ ID NO 23; 126pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising an HIV (human
 CC immunodeficiency virus) gp120 (envelope glycoprotein 120) amino acid
 CC sequence and its fragment from a breakthrough isolate HIV strain isolated
 CC from a vaccinee vaccinated with the first HIV gp120 polypeptide sequence
 CC comprises gp120 MN, gp120 A244, gp120 MN-GNE6 or gp120 MN-GNE8
 CC (recombinant gp120). Also included are an oligonucleotide of not more
 CC than 5 kilobases encoding the HIV gp120 polypeptide sequence, a vaccine
 CC comprising gp120 MN and the HIV gp120 polypeptide sequence (or fragment)
 CC in a suitable carrier and preparing an HIV vaccine (comprising adding an
 CC HIV gp120 polypeptide sequence or its fragments from a breakthrough
 CC isolate from a vaccinee to the vaccine with which the vaccinee was
 CC vaccinated). The composition and methods are useful for diagnosing,
 CC preventing or treating HIV infection (AIDS). NOTE: The authors have mixed
 CC up the SEQ ID numbers between the sequence listing and the
 CC description/claims, subsequently some sequences are claimed which may not
 CC have been intended to be claimed and some sequences which were intended
 CC to be claimed are not claimed, other sequences cannot be identified from
 CC the information given in the patent. The present sequence represents a
 CC gp120 protein from a breakthrough isolate HIV strain.
 XX
 SQ Sequence 469 AA;
 Query Match 80.0%; Score 36; DB 8; Length 469;
 Best Local Similarity 77.8%; Pred. No. 91;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FYSLKIVPI 9
 Db 140 FYKLIVPI 148
 ||| ||||
 RESULT 33
 AAW99862
 ID AAW99862 standard; peptide; 15 AA.
 XX
 AC AAW99862;
 XX
 XX 17-OCT-2003 (revised)
 DT 09-JUN-1999 (first entry)
 XX
 DE HIV-1 gp120 V1/V2 domain peptide p8.
 XX

KW HIV-1; gp120; V1/V2 domain; human immunodeficiency virus; epitope;
 KW infection; antibody; immunoassay.
 XX
 OS Human immunodeficiency virus 1.
 XX
 FN WO9912556-A1.
 FN
 PD 18-MAR-1999.
 XX
 PF 08-SEP-1998; 98WO-US018679.
 XX
 PR 08-SEP-1997; 97US-0058155P.
 XX
 PA (PUBL-) PUBLIC HEALTH RES INST NEW YORK.
 PA (PINT/) PINTER A.
 XX
 PI Pinter A;
 XX
 DR WPI; 1999-229137/19.
 XX
 PT New gp120 V1/V2 fusion proteins.
 XX
 PS Disclosure; Page 18; 64pp; English.
 XX
 CC The present invention describes a novel protein (A) comprising a gp120
 CC V1/V2 domain of an HIV-1 strain and not comprising the gp120 V3 domain of
 CC an HIV-1 strain, where the protein does not bind CD4, the gp120 V1/V2
 CC domain of the protein displaying an epitope which is recognized by an
 CC antibody which neutralizes at least one HIV-1 primary isolate with a ND90
 CC of at most 100 mu g/ml. The present sequence represents an HIV-1 gp120
 CC V1/V2 domain peptide from the present invention. The novel proteins can
 CC be used for stimulating the formation of antibodies capable of
 CC neutralizing infection by an HIV viral isolate in mammals. They can also
 CC be used for therapeutic treatment of subjects already infected with HIV.
 CC They can also be used in immunoassays for anti-HIV antibodies and for the
 CC production of anti-HIV antiserum. (Updated on 17-OCT-2003 to standardise
 CC OS field)
 XX
 SQ Sequence 15 AA;
 Query Match 77.8%; Score 35; DB 2; Length 15;
 Best Local Similarity 77.8%; Pred. No. 3,6;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FYSLKIVPI 9
 Db 5 FYKLIVPI 13
 ||| ||||
 RESULT 34
 AAW99851
 ID AAW99851 standard; peptide; 34 AA.
 XX
 AC AAW99851;
 XX
 DT 17-OCT-2003 (revised)
 DT 09-JUN-1999 (first entry)
 XX
 DE HIV-1 gp120 V1/V2 domain peptide #1.
 XX
 KW HIV-1; gp120; V1/V2 domain; human immunodeficiency virus; epitope;
 KW infection; antibody; immunoassay.
 XX
 OS Human immunodeficiency virus 1.
 XX
 FN WO9912556-A1.
 FN
 PD 18-MAR-1999.
 XX
 PF 08-SEP-1998; 98WO-US018679.
 XX
 PR 08-SEP-1997; 97US-0058155P.
 XX

PA (PUBL-) PUBLIC HEALTH RES INST NEW YORK.
 PA (PINT/) PINTER A.
 XX Pinter A;
 XX WPI; 1999-229137/19.
 XX New gp120 V1/V2 fusion proteins.
 XX Claim 11; Page 42; 64pp; English.
 XX The present invention describes a novel protein (A) comprising a gp120
 CC V1/V2 domain of an HIV-1 strain and not comprising the gp120 V3 domain of
 CC an HIV-1 strain, where the protein does not bind CD4, the gp120 V1/V2
 CC domain of the protein displaying an epitope which is recognized by an
 CC antibody which neutralizes at least one HIV-1 primary isolate with a ND90
 CC of at most 100 mu g/ml. The present sequence represents an HIV-1 gp120
 CC V1/V2 domain peptide from the present invention. The novel proteins can
 CC be used for stimulating the formation of antibodies capable of
 CC neutralizing infection by an HIV viral isolate in mammals. They can also
 CC be used for therapeutic treatment of subjects already infected with HIV.
 CC They can also be used in immunoassays for anti-HIV antibodies and for the
 CC production of anti-HIV antiserum. (Updated on 17-OCT-2003 to standardise
 CC OS field)
 XX Sequence 34 AA;
 SQ Query Match 77.8%; Score 35; DB 2; Length 34;
 Best Local Similarity 77.8%; Pred. No. 8.7;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FYSLXIVPI 9
 DB 25 FYKLDIVPI 33
 ||| ||||
 RESULT 35
 AAB10710
 ID AAB10710 standard; protein; 51 AA.
 AC AAB10710;
 XX 12-SEP-2003 (revised)
 DT 26-JAN-2001 (first entry)
 XX HIV-1 gp120 protein NL4-3 V2 loop region fragment.
 XX Viral protein; vaccine; anti-viral; anti-HIV; therapy; infection; gp120;
 KW V2 loop.
 KW Human immunodeficiency virus 1.
 OS WO200047223-A2.
 XX 17-AUG-2000.
 PD 03-DEC-1999; 99WO-EP009759.
 XX 12-FEB-1999; 99DE-01007485.
 XX (STPA-) STRATHMANN & CO AG.
 XX Schreiber M;
 PI WPI; 2000-549084/50.
 XX Viral vaccine comprises a mixture of protein sequence variants of a
 PT single viral protein, which is useful for prevention and therapy of viral
 PT infections, especially HIV, in humans.
 XX Disclosure; Fig 2a; 79pp; German.
 PS This invention describes a novel protein vaccine which comprises a

CC mixture of viral proteins, characterized in that the molecules are
 CC sequence variants of a single viral (partial) protein. The products of
 CC the invention have anti-viral and anti-HIV activity. Mixtures of
 CC structurally different viral proteins, that are sequence variants of a
 CC single protein are useful for production of vaccines for the prevention
 CC and/or therapy of viral infections in humans. The vaccines are especially
 CC useful for prevention and/or therapy of human immunodeficiency virus
 CC (HIV) infection in humans. The vectors and host cells are useful for the
 CC expression of the protein/DNA mixtures, which are also useful for
 CC preventing and/or therapy of viral infection. This sequence represents a
 CC HIV-1 gp120 protein V2 loop fragment. (Updated on 12-SEP-2003 to
 CC standardise OS field)
 XX Sequence 51 AA;
 SQ Query Match 77.8%; Score 35; DB 3; Length 51;
 Best Local Similarity 77.8%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FYSLXIVPI 9
 DB 25 FYKLDIVPI 33
 ||| ||||
 RESULT 36
 ABP52850
 ID ABP52850 standard; peptide; 78 AA.
 AC ABP52850;
 XX 29-AUG-2003 (revised)
 DT 02-NOV-2002 (first entry)
 XX HIV-1 gp120 V2 region related peptide SEQ ID NO:19.
 XX HIV; transgenic mouse; human monoclonal antibody; neutralising; HIV-1;
 KW gp120; anti-HIV; gene therapy; antibody; glycoprotein 120; infection.
 XX Human immunodeficiency virus 1.
 OS WO200259154-A2.
 XX 01-AUG-2002.
 PD 25-JAN-2002; 2002WO-US002171.
 XX 26-JAN-2001; 2001US-0264398P.
 PR 02-FEB-2001; 2001US-0266106P.
 PR 03-FEB-2001; 2001US-0265984P.
 PR 21-FEB-2001; 2001US-0270466P.
 XX (ABGE-) ABGENIX INC.
 PA (PUBL-) PUBLIC HEALTH RES INST.
 XX Pinter A, He Y, Corvalan JR;
 PI WPI; 2002-627409/67.
 XX Isolated human antibody or its antigen-binding portion that specifically
 PT binds to human deficiency virus-1 glycoprotein 120 and that has HIV-1
 PT neutralizing activity, useful to treat or prevent HIV-1 infection.
 XX Disclosure; Page 12; 163pp; English.
 XX The present invention describes an isolated human antibody (I) or its
 CC antigen-binding portion that specifically binds to human immunodeficiency
 CC virus (HIV)-1 glycoprotein (gp)120 protein and that has HIV-1
 CC neutralising activity, where (I) or its antigen-binding portion
 CC recognises an epitope on a V1/V2 domain of HIV-1 gp120, where the epitope
 CC is dependent on the presence of a sequence in the V1 loop. (I) has anti-
 CC HIV activity and can be used in gene therapy. (I) is useful for treating,
 CC preventing or inhibiting HIV-1 infection in a subject or for preventing
 CC or lessening the severity of a condition caused by HIV-1 infection in a

CC subject, by administering (I) to the subject. (I) is useful for
CC inhibiting HIV-1 virus binding to a T-cell, or for inhibiting HIV-1 virus
CC infection of a T-cell, by contacting the virus with (I). (I) is useful
CC for inhibiting HIV-1 gp120-mediated binding by contacting a gp120-
CC expressing HIV-1 virus with (I). (I) is useful diagnostically to detect
CC the presence of HIV-1 virus in a subject. The present sequence represents
CC an HIV-1 V2 region related peptide, which is used in the exemplification
CC of the present invention. (Updated on 29-AUG-2003 to standardise OS
CC field)
XX
SQ Sequence 78 AA;

Query Match 77.8%; Score 35; DB 5; Length 78;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 56 FYKLDIVPI 64

RESULT 37
AAW99852
ID AAW99852 standard; peptide; 96 AA.
XX
AC AAW99852;
XX
DT 17-OCT-2003 (revised)
DT 09-JUN-1999 (first entry)
XX
XX HIV-1 gp120 V1/V2 domain peptide SEQ ID NO:1.
DE
XX
KW HIV-1; gp120; V1/V2 domain; human immunodeficiency virus; epitope;
KW infection; antibody; immunoassay.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9912556-A1.
XX
PD 18-MAR-1999.
XX
PF 08-SEP-1998; 98WO-US018679.
XX
PR 08-SEP-1997; 97US-0058155P.
XX
PA (PUBL-) PUBLIC HEALTH RES INST NEW YORK.
PA (PINT/) PINTER A.
XX
PI Pinter A;
XX
DR WPI; 1999-229137/19.
XX
PT New gp120 V1/V2 fusion proteins.
XX
PS Claim 14; Page 42; 64pp; English.

CC The present invention describes a novel protein (A) comprising a gp120
CC V1/V2 domain of an HIV-1 strain and not comprising the gp120 V3 domain of
CC an HIV-1 strain, where the protein does not bind CD4, the gp120 V1/V2
CC domain of the protein displaying an epitope which is recognized by an
CC antibody which neutralizes at least one HIV-1 primary isolate with a ND90
CC of at most 100 mu g/ml. The present sequence represents an HIV-1 gp120
CC V1/V2 domain peptide from the present invention. The novel proteins can
CC be used for stimulating the formation of antibodies capable of
CC neutralizing infection by an HIV viral isolate in mammals. They can also
CC be used for therapeutic treatment of subjects already infected with HIV.
CC They can also be used in immunoassays for anti-HIV antibodies and for the
CC production of anti-HIV antiserum. (Updated on 17-OCT-2003 to standardise
CC OS field)
XX
SQ Sequence 96 AA;

Query Match 77.8%; Score 35; DB 2; Length 96;

Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 66 FYKLDIVPI 74

RESULT 38
ABP78185
ID ABP78185 standard; protein; 245 AA.
XX
AC ABP78185;
XX
DT 07-MAR-2003 (first entry)
XX
DE N. gonorrhoeae amino acid sequence SEQ ID 2900.
XX
KW Antibacterial; infection; vaccine; gene therapy.
XX
OS Neisseria gonorrhoeae.
XX
PN WO200279243-A2.
XX
PD 10-OCT-2002.
XX
PF 12-FEB-2002; 2002WO-IB002069.
XX
PR 12-FEB-2001; 2001GB-00003424.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Fontana MR, Pizza M, Massignani V, Monaci E;
XX
DR WPI; 2003-058415/05.
DR N-PSDB; ABZ39155.
XX
PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a
PT medicament for treating or preventing N. gonorrhoeae infection.
XX
PS Disclosure; Page 400; 815pp; English.

CC The present invention relates to proteins from Neisseria gonorrhoeae.
CC Also disclosed are the nucleic acid molecules encoding the proteins and
CC antibodies that specifically bind to the proteins. The composition
CC comprising the protein, nucleic acid or antibody is useful for the
CC manufacture of a medicament for treating or preventing N. gonorrhoeae
CC infection, this may be in the form of a vaccine or gene therapy.
CC Sequences given in records ABP76736-ABP81046 represent nucleic acid
CC molecules of the invention
XX
SQ Sequence 245 AA;

Query Match 77.8%; Score 35; DB 6; Length 245;
Best Local Similarity 55.6%; Pred. No. 73;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 179 FYSPKLLPV 187

RESULT 39
ABU37576
ID ABU37576 standard; protein; 245 AA.
XX
AC ABU37576;
XX
DT 23-OCT-2003 (revised)
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #23103.

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX Neisseria gonorrhoeae.
XX WO200277183-A2.
PN
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR N-PSDB; ACA11446.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 65500; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway;
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 245 AA;

Query Match 77.8%; Score 35; DB 6; Length 245;
Best Local Similarity 55.6%; Pred. No. 73;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
||| |::|
DB 179 FYSFKLLPV 187

RESULT 40

ADP08243
ID ADP08243 standard; protein; 245 AA.

XX
AC ADP08243;

XX
DT 26-AUG-2004 (first entry)

XX
DE Neisseria meningitidis MC58 OMV-related membrane protein - SEQ ID 76.

XX
KW outer-membrane vesicle; antibacterial; antiinflammatory;
KW meningococcal protein trafficking; localisation; infection; vaccine;
KW gene therapy.

XX
OS Neisseria meningitidis MC58.

XX
PN WO2004046177-A2.

XX
PD 03-JUN-2004.

XX
PF 17-NOV-2003; 2003WO-IB006281.

XX
PR 15-NOV-2002; 2002GB-00026734.

XX
PR 27-MAR-2003; 2003GB-00007131.

XX
PA (CHTR) CHIRON SRL.

XX
PI Norais N, Grandi G;

XX
DR WPI; 2004-420615/39.

XX
PT New compositions having outer-membrane vesicles and proteins from
PT Neisseria meningitidis, useful in the field of meningococcal
PT biochemistry, in particular for preventing and/or treating meningococcal
PT infections.

XX
PS Claim 9; SEQ ID NO 76; 79pp; English.

XX
CC The invention relates to a novel composition comprising outer-membrane
CC vesicles (OMV) prepared from a first strain of *Neisseria meningitidis* and
CC 1 or more proteins which are present in OMVs prepared from a second
CC strain of *N. meningitidis*, but which are not present in OMVs prepared
CC from the first strain. The composition of the invention demonstrates
CC antibacterial and antiinflammatory activities and may be useful in the
CC field of meningococcal biochemistry, in particular the trafficking and
CC localisation of meningococcal proteins, as well as in the prevention or
CC treatment of meningococcal infections, possibly via the production of a
CC vaccine or gene therapy. The current sequence is that of a *Neisseria*
CC meningitidis MC58 outer-membrane vesicle (OMV)-related membrane protein
CC of the invention.

XX
SQ Sequence 245 AA;

Query Match 77.8%; Score 35; DB 8; Length 245;
Best Local Similarity 55.6%; Pred. No. 73;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
||| |::|
DB 179 FYSFKLLPV 187

Search completed: February 24, 2005, 19:11:39
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OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-914-205-5

Perfect score: 45

Sequence: 1 FYSLKIVPI 9

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Total number of hits satisfying chosen parameters: 513545

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgn2_6/prodata/1/iaa/ECTUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	9	US-09-256-194-5	Sequence 5, Appl
2	39	86.7	43	US-09-536-977-6	Sequence 6, Appl
3	39	86.7	168	US-09-536-977-42	Sequence 42, Appl
4	39	86.7	425	US-09-536-977-46	Sequence 46, Appl
5	39	86.7	425	US-09-536-977-48	Sequence 48, Appl
6	39	86.7	425	US-09-536-977-50	Sequence 50, Appl
7	39	86.7	425	US-09-536-977-52	Sequence 52, Appl
8	39	86.7	476	US-09-536-977-74	Sequence 74, Appl
9	39	86.7	635	US-09-536-977-68	Sequence 68, Appl
10	39	86.7	657	US-09-256-194-2	Sequence 2, Appl
11	39	86.7	687	US-09-536-977-70	Sequence 70, Appl
12	39	86.7	820	US-09-536-977-72	Sequence 72, Appl
13	38	84.4	498	US-08-889-841B-2	Sequence 2, Appl
14	38	84.4	498	US-08-889-841B-5	Sequence 5, Appl
15	38	84.4	498	US-09-419-362-2	Sequence 2, Appl
16	38	84.4	498	US-09-419-362-5	Sequence 5, Appl
17	36	80.0	131	US-09-513-999C-5328	Sequence 5328, Ap
18	36	80.0	454	US-09-949-016-11717	Sequence 11717, A
19	36	80.0	469	US-08-889-841B-23	Sequence 23, Appl
20	36	80.0	469	US-09-419-362-23	Sequence 23, Appl
21	35	77.8	15	US-10-038-407-16	Sequence 16, Appl
22	35	77.8	34	US-10-038-407-2	Sequence 2, Appl
23	35	77.8	96	US-10-038-407-1	Sequence 1, Appl
24	35	77.8	365	US-10-038-407-28	Sequence 28, Appl
25	35	77.8	473	US-09-438-917-6	Sequence 6, Appl
26	35	77.8	494	US-08-889-841B-19	Sequence 19, Appl
27	35	77.8	494	US-09-419-362-19	Sequence 19, Appl

28 35 77.8 495 3 US-08-889-841B-25 Sequence 25, Appl
29 35 77.8 495 3 US-08-889-841B-28 Sequence 28, Appl
30 35 77.8 495 4 US-09-419-362-25 Sequence 25, Appl
31 35 77.8 495 4 US-09-419-362-28 Sequence 28, Appl
32 35 77.8 587 4 US-09-646-028-50 Sequence 50, Appl
33 35 77.8 595 4 US-09-646-028-56 Sequence 56, Appl
34 35 77.8 601 4 US-09-646-028-52 Sequence 52, Appl
35 35 77.8 826 1 US-08-375-510-2 Sequence 2, Appl
36 35 77.8 826 2 US-08-487-657-2 Sequence 2, Appl
37 35 77.8 854 4 US-09-309-572-23 Sequence 23, Appl
38 35 77.8 854 4 US-09-718-096-23 Sequence 23, Appl
39 34 75.6 28 2 US-08-493-235-13 Sequence 13, Appl
40 34 75.6 28 4 US-10-038-407-6 Sequence 6, Appl
41 34 75.6 93 4 US-10-038-407-3 Sequence 3, Appl
42 34 75.6 99 4 US-09-248-796A-22816 Sequence 22816, A
43 34 75.6 358 4 US-09-438-917-19 Sequence 19, Appl
44 34 75.6 429 4 US-09-438-917-16 Sequence 16, Appl
45 34 75.6 455 3 US-08-889-841B-46 Sequence 46, Appl

ALIGNMENTS

RESULT 1

US-09-256-194-5
; Sequence 5, Application US/09256194
; Patent No. 6395714
; GENERAL INFORMATION:
; APPLICANT: Sia, Charles D.Y.
; APPLICANT: Cao, Shi Xian
; APPLICANT: Persson, Roy
; APPLICANT: Rovinski, Benjamin
; TITLE OF INVENTION: EXPRESSING GP140 FRAGMENT OF PRIMARY HIV-1 ISOLATE
; FILE REFERENCE: 1038-920
; CURRENT APPLICATION NUMBER: US/09/256,194
; CURRENT FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-256-194-5

Query Match 100.0%; Score 45; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9

Db 1 FYSLKIVPI 9

RESULT 2

US-09-536-977-6
; Sequence 6, Application US/09536977
; Patent No. 6649409
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT
; TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; TITLE OF INVENTION: BX08 CONSTRUCTS
; FILE REFERENCE: 030307/0169
; CURRENT APPLICATION NUMBER: US/09/536,977
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/128,558
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: DK PA1999 00427
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6

```
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-536-977-6

Query Match      86.7%; Score 39; DB 4; Length 43;
Best Local Similarity 88.9%; Pred. No. 0.44;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      20 FYSLDIVPI 28

RESULT 3
US-09-536-977-42
; Sequence 42, Application US/09536977
; Patent No. 6649409
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT
; TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; FILE REFERENCE: 030307/0169
; CURRENT APPLICATION NUMBER: US/09/536,977
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/128,558
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: DK PA1999 00427
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-536-977-42

Query Match      86.7%; Score 39; DB 4; Length 168;
Best Local Similarity 88.9%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      145 FYSLDIVPI 153

RESULT 4
US-09-536-977-46
; Sequence 46, Application US/09536977
; Patent No. 6649409
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT
; TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; FILE REFERENCE: 030307/0169
; CURRENT APPLICATION NUMBER: US/09/536,977
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/128,558
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: DK PA1999 00427
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-536-977-46

Query Match      86.7%; Score 39; DB 4; Length 425;
Best Local Similarity 88.9%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      145 FYSLDIVPI 153

RESULT 5
US-09-536-977-48
; Sequence 48, Application US/09536977
; Patent No. 6649409
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT
; TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; FILE REFERENCE: 030307/0169
; CURRENT APPLICATION NUMBER: US/09/536,977
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/128,558
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: DK PA1999 00427
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-536-977-48

Query Match      86.7%; Score 39; DB 4; Length 425;
Best Local Similarity 88.9%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      145 FYSLDIVPI 153

RESULT 6
US-09-536-977-50
; Sequence 50, Application US/09536977
; Patent No. 6649409
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT
; TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; FILE REFERENCE: 030307/0169
; CURRENT APPLICATION NUMBER: US/09/536,977
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/128,558
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: DK PA1999 00427
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-536-977-50

Query Match      86.7%; Score 39; DB 4; Length 425;
Best Local Similarity 88.9%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      145 FYSLDIVPI 153

RESULT 7
US-09-536-977-52
; Sequence 52, Application US/09536977
; Patent No. 6649409
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; TITLE OF INVENTION: METHOD FOR PRODUCING A NUCLEOTIDE SEQUENCE CONSTRUCT
; TITLE OF INVENTION: WITH OPTIMIZED CODONS FOR AN HIV GENETIC VACCINE BASED
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; TITLE OF INVENTION: ON A PRIMARY, EARLY HIV ISOLATE AND SYNTHETIC ENVELOPE
; FILE REFERENCE: 030307/0169
; CURRENT APPLICATION NUMBER: US/09/536,977
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/128,558
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: DK PA1999 00427
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-536-977-52

Query Match      86.7%; Score 39; DB 4; Length 425;
Best Local Similarity 88.9%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      145 FYSLDIVPI 153
```



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Db      156 FYSLDVVP1 164

RESULT 16
US-09-419-362-5
; Patent No. 6585979
; GENERAL INFORMATION:
; APPLICANT: Beriman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/09/419,362
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 498
; TYPE: PRT
; ORGANISM: HIV
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(498)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-419-362-5

Query Match      84.4%; Score 38; DB 4; Length 498;
Best Local Similarity 77.8%; Pred. No. 9.6;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVP1 9
Db      156 FYSLDVVP1 164

RESULT 17
US-09-513-999C-5328
; Sequence 5328, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5328
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5328

Query Match      80.0%; Score 36; DB 4; Length 131;
Best Local Similarity 75.0%; Pred. No. 6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVP 8
Db      13 FYSLKVP 20

RESULT 18
US-09-949-016-11717
; Sequence 11717, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11717
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11717

Query Match      80.0%; Score 36; DB 4; Length 454;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVP 8
Db      14 FYSLKVP 21

RESULT 19
US-08-889-841B-23
; Sequence 23, Application US/08889841B
; GENERAL INFORMATION:
; APPLICANT: Beriman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703CIP
; CURRENT APPLICATION NUMBER: US/08/889,841B
; CURRENT FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 469
; TYPE: PRT
; ORGANISM: HIV
US-08-889-841B-23

Query Match      80.0%; Score 36; DB 3; Length 469;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FYSLKIVP1 9
Db      140 FYKLNIVP1 148

RESULT 20
US-09-419-362-23
; Sequence 23, Application US/09419362
; Patent No. 6585979
; GENERAL INFORMATION:
; APPLICANT: Beriman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/09/419,362
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
```

```
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 469
; TYPE: PRT
; ORGANISM: HIV
US-09-419-362-23

Query Match      80.0%; Score 36; DB 4; Length 469;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
Db 140 FYKLDIVPI 148

RESULT 21
US-10-038-407-16
; Sequence 16, Application US/10038407
; Patent No. 6815201
; GENERAL INFORMATION:
; APPLICANT: Pinter, Abraham
; TITLE OF INVENTION: HIV-1 gp120 V1/V2 DOMAIN EPITOPES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/18679
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-16

Query Match      77.8%; Score 35; DB 4; Length 15;
Best Local Similarity 77.8%; Pred. No. 0.96;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
Db 5 FYKLDIVPI 13

RESULT 22
US-10-038-407-2
; Sequence 2, Application US/10038407
; Patent No. 6815201
; GENERAL INFORMATION:
; APPLICANT: Pinter, Abraham
; TITLE OF INVENTION: HIV-1 gp120 V1/V2 DOMAIN EPITOPES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/18679
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-2

Query Match      77.8%; Score 35; DB 4; Length 34;
Best Local Similarity 77.8%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
Db 25 FYKLDIVPI 33

RESULT 23
US-10-038-407-1
; Sequence 1, Application US/10038407
; Patent No. 6815201
; GENERAL INFORMATION:
; APPLICANT: Pinter, Abraham
; TITLE OF INVENTION: HIV-1 gp120 V1/V2 DOMAIN EPITOPES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/18679
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-1

Query Match      77.8%; Score 35; DB 4; Length 96;
Best Local Similarity 77.8%; Pred. No. 7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
Db 66 FYKLDIVPI 74

RESULT 24
US-10-038-407-28
; Sequence 28, Application US/10038407
; Patent No. 6815201
; GENERAL INFORMATION:
; APPLICANT: Pinter, Abraham
; TITLE OF INVENTION: HIV-1 gp120 V1/V2 DOMAIN EPITOPES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/18679
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-28

Query Match      77.8%; Score 35; DB 4; Length 365;
Best Local Similarity 77.8%; Pred. No. 29;
```

```
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 FYSLKIVPI 9
Db 335 FYKLDIVPI 343

RESULT 25
US-09-438-917-6
; Sequence 6, Application US/09438917
; Patent No. 6787646
; GENERAL INFORMATION:
; APPLICANT: Immunol Incorporated
; APPLICANT: Welch, Peter J.
; APPLICANT: Barber, Jack R.
; TITLE OF INVENTION: Tumor Suppressor Molecules and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: 039316-0301
; CURRENT APPLICATION NUMBER: US/09/438,917
; CURRENT FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 473
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-438-917-6

Query Match 77.8%; Score 35; DB 4; Length 473;
Best Local Similarity 62.5%; Pred. No. 38;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 YSLKIVPI 9
Db 197 YSIKVVP 204

RESULT 26
US-08-889-841B-19
; Sequence 19, Application US/08889841B
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703CIP
; CURRENT APPLICATION NUMBER: US/08/889,841B
; CURRENT FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 494
; TYPE: PRT
; ORGANISM: HIV
US-08-889-841B-19

Query Match 77.8%; Score 35; DB 3; Length 494;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 FYSLKIVPI 9
Db 145 FYKLDIVPI 153

RESULT 27
US-09-419-362-19
; Sequence 19, Application US/09419362
; Patent No. 6585979
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
```

```
; CURRENT APPLICATION NUMBER: US/09/419,362
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 494
; TYPE: PRT
; ORGANISM: HIV
US-09-419-362-19

Query Match 77.8%; Score 35; DB 4; Length 494;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 FYSLKIVPI 9
Db 145 FYKLDIVPI 153

RESULT 28
US-08-889-841B-25
; Sequence 25, Application US/08889841B
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703CIP
; CURRENT APPLICATION NUMBER: US/08/889,841B
; CURRENT FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 495
; TYPE: PRT
; ORGANISM: HIV
US-08-889-841B-25

Query Match 77.8%; Score 35; DB 3; Length 495;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 FYSLKIVPI 9
Db 152 FYKLDIVPI 160

RESULT 29
US-08-889-841B-28
; Sequence 28, Application US/08889841B
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703CIP
; CURRENT APPLICATION NUMBER: US/08/889,841B
; CURRENT FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 495
; TYPE: PRT
; ORGANISM: HIV
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(495)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-08-889-841B-28
```

Query Match 77.8%; Score 35; DB 3; Length 495;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
||| ||||
DB 152 FYKLDIVPI 160

RESULT 30
US-09-419-362-25
; Sequence 25, Application US/09419362
; Patent No. 6585979
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/09/419,362
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 495
; TYPE: PRT
; ORGANISM: HIV
US-09-419-362-25

Query Match 77.8%; Score 35; DB 4; Length 495;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
||| ||||
DB 152 FYKLDIVPI 160

RESULT 31
US-09-419-362-28
; Sequence 28, Application US/09419362
; Patent No. 6585979
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/09/419,362
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 495
; TYPE: PRT
; ORGANISM: HIV
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(495)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-419-362-28

Query Match 77.8%; Score 35; DB 4; Length 495;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
||| ||||

DB 152 FYKLDIVPI 160

RESULT 32
US-09-646-028-50
; Sequence 50, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 587
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-50

Query Match 77.8%; Score 35; DB 4; Length 587;
Best Local Similarity 77.8%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
||| ||||
DB 248 FYKLDIVPI 256

RESULT 33
US-09-646-028-56
; Sequence 56, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-56

Query Match 77.8%; Score 35; DB 4; Length 595;
Best Local Similarity 77.8%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
||| ||||
DB 256 FYKLDIVPI 264

RESULT 34
US-09-646-028-52
; Sequence 52, Application US/09646028
; Patent No. 6562347

GENERAL INFORMATION:
APPLICANT: Kwak, Larry
APPLICANT: Birsgyn, Atya
TITLE OF INVENTION: CHEMOKINES-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 52
LENGTH: 601
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-52

Query Match 77.8%; Score 35; DB 4; Length 601;
Best Local Similarity 77.8%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
DB 262 FYKLDIVPI 270

RESULT 35
US-08-375-510-2
Sequence 2, Application US/08375510
Patent No. 5576421
GENERAL INFORMATION:
APPLICANT: Saito, Atsushi
APPLICANT: Sinagawa, Hideo
APPLICANT: Nakata, Atsuo
TITLE OF INVENTION: HIV ANTIGEN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch and Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/375,510
FILING DATE: 04-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/985,949
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 216-309P
TELEPHONE: (703) 241-1300
TELEFAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-375-510-2

Query Match 77.8%; Score 35; DB 1; Length 826;
Best Local Similarity 77.8%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
DB 148 FYKLDIVPI 156

RESULT 36
US-08-487-657-2
Sequence 2, Application US/08487657
Patent No. 5834267
GENERAL INFORMATION:
APPLICANT: Saito, Atsushi
APPLICANT: Sinagawa, Hideo
APPLICANT: Nakata, Atsuo
TITLE OF INVENTION: HIV ANTIGEN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch and Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/487,657
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/375,510
FILING DATE: 18-JAN-1995
APPLICATION NUMBER: US/07/985,949
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 216-309P
TELEPHONE: (703) 241-1300
TELEFAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-487-657-2

Query Match 77.8%; Score 35; DB 2; Length 826;
Best Local Similarity 77.8%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
DB 148 FYKLDIVPI 156

RESULT 37

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US-09-309-572-23
; Sequence 23, Application US/09309572
; Patent No. 6440730
; GENERAL INFORMATION:
; APPLICANT: Heinrich-Pette-Institut
; TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV
; FILE REFERENCE: P50489
; CURRENT APPLICATION NUMBER: US/09/309,572
; CURRENT FILING DATE: 1999-05-11
; EARLIER APPLICATION NUMBER: DE 198 56 463
; EARLIER FILING DATE: 1998-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: envelope polyprotein
US-09-309-572-23
Query Match 77.8%; Score 35; DB 4; Length 854;
Best Local Similarity 77.8%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 176 FYKLDIVPI 184

RESULT 38
US-09-718-096-23
; Sequence 23, Application US/09718096
; Patent No. 6589763
; GENERAL INFORMATION:
; APPLICANT: Von Laer, Meike-Dorothee
; TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV
; FILE REFERENCE: 35-195
; CURRENT APPLICATION NUMBER: US/09/718,096
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: DE 19856463.5
; PRIOR FILING DATE: 1998-11-26
; PRIOR APPLICATION NUMBER: EP 99250415.9
; PRIOR FILING DATE: 1999-11-25
; PRIOR APPLICATION NUMBER: US 09/309,572
; PRIOR FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: envelope polyprotein
US-09-718-096-23
Query Match 77.8%; Score 35; DB 4; Length 854;
Best Local Similarity 77.8%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 176 FYKLDIVPI 184

RESULT 39
US-08-493-235-13
; Sequence 13, Application US/08493235
; Patent No. 5840313
; GENERAL INFORMATION:
; APPLICANT: Vahne, Anders
; APPLICANT: Svennerholm, Bo
; APPLICANT: Rymo, Lars
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US-10-038-407-6

Query Match 75.6%; Score 34; DB 4; Length 28;
 Best Local Similarity 66.7%; Pred. No. 3;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FYSLKIVPI 9
 Db 19 FYKLDVPI 27

Search completed: February 24, 2005, 19:16:10
 Job time : 43 secs

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OM protein - protein search, using sw model

Run on: February 24, 2005, 19:14:48 ; Search time 131 Seconds
(without alignments)
22.482 Million cell updates/sec

Title: US-09-914-205-5
Perfect score: 45
Sequence: 1 FVSLKIVPI 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pcp:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pcp:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp:*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pcp:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp:*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	91.1	765	US-10-437-963-112846	Sequence 112846,
2	38	84.4	485	US-10-866-527-48	Sequence 48, Appl
3	38	84.4	498	US-10-371-472-2	Sequence 2, Appl
4	38	84.4	498	US-10-371-472-5	Sequence 5, Appl
5	36	80.0	169	US-09-925-299-1125	Sequence 1125, Ap
6	36	80.0	169	US-09-925-299-1125	Sequence 1125, Ap
7	36	80.0	210	US-09-925-300-1354	Sequence 1354, Ap
8	36	80.0	453	US-09-935-642-8	Sequence 8, Appl
9	36	80.0	453	US-10-205-331-40	Sequence 40, Appl
10	36	80.0	453	US-10-408-765A-521	Sequence 521, App
11	36	80.0	453	US-10-408-765A-2214	Sequence 2214, Ap
12	36	80.0	453	US-10-408-765A-2215	Sequence 2215, Ap
13	36	80.0	469	US-10-371-472-23	Sequence 23, Appl

14	35	77.8	15	14	US-10-038-407-16	Sequence 16, Appl
15	35	77.8	34	14	US-10-038-407-2	Sequence 2, Appl
16	35	77.8	96	14	US-10-038-407-1	Sequence 1, Appl
17	35	77.8	245	15	US-10-282-122A-65500	Sequence 65500, A
18	35	77.8	278	15	US-10-264-237-1845	Sequence 1845, Ap
19	35	77.8	365	14	US-10-038-407-28	Sequence 28, Appl
20	35	77.8	468	17	US-10-866-527-24	Sequence 24, Appl
21	35	77.8	484	17	US-10-866-527-2	Sequence 2, Appl
22	35	77.8	486	17	US-10-866-527-102	Sequence 102, App
23	35	77.8	488	17	US-10-866-527-72	Sequence 72, Appl
24	35	77.8	490	17	US-10-866-527-56	Sequence 56, Appl
25	35	77.8	494	15	US-10-371-472-19	Sequence 19, Appl
26	35	77.8	495	15	US-10-371-472-25	Sequence 25, Appl
27	35	77.8	495	15	US-10-371-472-28	Sequence 28, Appl
28	35	77.8	503	9	US-09-753-841-4	Sequence 4, Appl
29	35	77.8	509	17	US-10-866-527-114	Sequence 114, App
30	35	77.8	511	17	US-10-866-527-94	Sequence 94, Appl
31	35	77.8	515	16	US-10-462-040A-49	Sequence 49, Appl
32	35	77.8	518	16	US-10-462-040A-45	Sequence 45, Appl
33	35	77.8	518	16	US-10-462-040A-46	Sequence 46, Appl
34	35	77.8	518	16	US-10-462-040A-47	Sequence 47, Appl
35	35	77.8	518	16	US-10-462-040A-48	Sequence 48, Appl
36	35	77.8	587	14	US-10-335-394-50	Sequence 50, Appl
37	35	77.8	595	14	US-10-335-394-56	Sequence 56, Appl
38	35	77.8	601	14	US-10-335-394-52	Sequence 52, Appl
39	35	77.8	795	9	US-09-254-783A-1	Sequence 1, Appl
40	35	77.8	795	13	US-10-152-058-1	Sequence 1, Appl
41	34	75.6	20	9	US-09-775-805-63	Sequence 63, Appl
42	34	75.6	20	16	US-10-753-339-63	Sequence 63, Appl
43	34	75.6	28	14	US-10-038-407-6	Sequence 6, Appl
44	34	75.6	30	9	US-09-775-805-23	Sequence 23, Appl
45	34	75.6	30	16	US-10-753-339-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1

US-10-437-963-112846
; Sequence 112846, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 112846
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_16692C.1.pcp
US-10-437-963-112846

Query Match 91.1% Score 41; DB 16; Length 765;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 99 FVSLKILPV 107

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RESULT 2
US-10-866-527-48
; Sequence 48, Application US/10866527
; Publication No. US20050025779A1
; GENERAL INFORMATION:
; APPLICANT: VaxGen, Inc.
; APPLICANT: Berman, Phillip W
; APPLICANT: Jobsen, David V
; TITLE OF INVENTION: HIV-1 ENVELOPE GLYCOPROTEINS HAVING UNUSUAL DISULFIDE STRUCTURE
; FILE REFERENCE: 409J-000210US
; CURRENT APPLICATION NUMBER: US/10/866,527
; CURRENT FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-866-527-48
Query Match      84.4%; Score 38; DB 17; Length 485;
Best Local Similarity 77.8%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
Db      152 FYSLDVVP 160

RESULT 3
US-10-371-472-2
; Sequence 2, Application US/10371472
; Publication No. US20040052821A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/10/371,472
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/419,362
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 498
; TYPE: PRT
; ORGANISM: HIV
US-10-371-472-2
Query Match      84.4%; Score 38; DB 15; Length 498;
Best Local Similarity 77.8%; Pred. No. 36;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 FYSLKIVPI 9
Db      156 FYSLDVVP 164

RESULT 4
US-10-371-472-5
; Sequence 5, Application US/10371472
; Publication No. US20040052821A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/10/371,472
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/419,362
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 498
; TYPE: PRT
; ORGANISM: HIV
US-10-371-472-5
Query Match      84.4%; Score 38; DB 15; Length 498;
Best Local Similarity 77.8%; Pred. No. 36;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 FYSLKIVPI 9
Db      156 FYSLDVVP 164

RESULT 5
US-09-925-299-1125
; Sequence 1125, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1125
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-1125
Query Match      80.0%; Score 36; DB 9; Length 169;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 FYSLKIVP 8
Db      14 FYSLKVP 21

RESULT 6
US-09-925-299-1125
; Sequence 1125, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
US-09-925-299-1125
Query Match      80.0%; Score 36; DB 9; Length 169;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY      1 FYSLKIVP 8
Db      14 FYSLKVP 21
```

```
; SEQ ID NO 1125
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-1125

Query Match      80.0%; Score 36; DB 10; Length 169;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVP 8
Db 14 FYSLKVAP 21

RESULT 7
US-09-925-300-1354
; Sequence 1354, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1354
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (192)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (208)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1354

Query Match      80.0%; Score 36; DB 9; Length 210;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVP 8
Db 14 FYSLKVAP 21

RESULT 8
US-09-935-642-8
; Sequence 8, Application US/09935642
; Publication No. US20030044795A1
; GENERAL INFORMATION:
; APPLICANT: BYRJALSEN, Inger
; APPLICANT: LARSEN, Peter
; APPLICANT: STEPHEN, John
; TITLE OF INVENTION: Biochemical Markers for the Human
; TITLE OF INVENTION: Endometrium
; FILE REFERENCE: 8969-014
; CURRENT APPLICATION NUMBER: US/09/935,642
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: PCT/GB97/02394
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: PCT/GB9707132.8
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: PCT/GB9618600.2
; PRIOR FILING DATE: 1996-09-06
```

```
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-642-8

Query Match      80.0%; Score 36; DB 10; Length 453;
Best Local Similarity 75.0%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVP 8
Db 13 FYSLKVAP 20

RESULT 9
US-10-205-331-40
; Sequence 40, Application US/10205331
; Publication No. US20040058326A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Finnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018199
; CURRENT APPLICATION NUMBER: US/10/205,331
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Core protein II of human mitochondrial cytochrome bc-1 complex
US-10-205-331-40

Query Match      80.0%; Score 36; DB 15; Length 453;
Best Local Similarity 75.0%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVP 8
Db 13 FYSLKVAP 20

RESULT 10
US-10-408-765A-521
; Sequence 521, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 521
; LENGTH: 453
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-521

Query Match      80.0%; Score 36; DB 16; Length 453;
Best Local Similarity 75.0%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVP 8
DB      13 FYSLKVP 20

RESULT 11
US-10-408-765A-2214
; Sequence 2214, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2214
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2214

Query Match      80.0%; Score 36; DB 16; Length 453;
Best Local Similarity 75.0%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVP 8
DB      13 FYSLKVP 20

RESULT 12
US-10-408-765A-2215
; Sequence 2215, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2215
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2215

Query Match      80.0%; Score 36; DB 16; Length 453;
```

```
Best Local Similarity 75.0%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVP 8
DB      13 FYSLKVP 20

RESULT 13
US-10-371-472-23
; Sequence 23, Application US/10371472
; Publication No. US20040052821A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/10/371,472
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/419,362
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 469
; TYPE: PRT
; ORGANISM: HIV
US-10-371-472-23

Query Match      80.0%; Score 36; DB 15; Length 469;
Best Local Similarity 77.8%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
DB      140 FYKLNIVPI 148

RESULT 14
US-10-038-407-16
; Sequence 16, Application US/10038407
; Publication No. US20030105282A1
; GENERAL INFORMATION:
; APPLICANT: Pinter, Abraham
; TITLE OF INVENTION: HIV-1 gp120 V1/V2 DOMAIN EPITOPES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/186679
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-16

Query Match      77.8%; Score 35; DB 14; Length 15;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
DB      5 FYKLDIVPI 13
```

```
RESULT 15
US-10-038-407-2
; Sequence 2, Application US/10038407
; Publication NO. US20030105282A1
; GENERAL INFORMATION:
; APPLICANT: Pinter, Abraham
; TITLE OF INVENTION: HIV-1 gp120 V1/V2 DOMAIN EPITOPES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/18679
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-2
Query Match      77.8%; Score 35; DB 14; Length 34;
Best Local Similarity 77.8%; Pred. No. 8.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
      ||| |||||
DB      25 FYKLDIVPI 33

RESULT 16
US-10-038-407-1
; Sequence 1, Application US/10038407
; Publication NO. US20030105282A1
; GENERAL INFORMATION:
; APPLICANT: Pinter, Abraham
; TITLE OF INVENTION: CAPABLE OF GENERATING NEUTRALIZING ANTIBODIES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/18679
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-1
Query Match      77.8%; Score 35; DB 14; Length 96;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
      ||| |||||
DB      66 FYKLDIVPI 74

RESULT 17
US-10-282-122A-65500
; Sequence 65500, Application US/10282122A
```

```
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65500
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-282-122A-65500
Query Match      77.8%; Score 35; DB 15; Length 245;
Best Local Similarity 55.6%; Pred. No. 69;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 FYSLKIVPI 9
      ||| |||||
DB      179 FYSFKLLPV 187

RESULT 18
US-10-264-237-1845
; Sequence 1845, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1845
```

```
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (234)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (244)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (247)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (262)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-1845
```

```
Query Match 77.8%; Score 35; DB 15; Length 278;
Best Local Similarity 62.5%; Pred. No. 79;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 YSLKIVPI 9
Db 197 YSIKVVPI 204
```

```
RESULT 19
US-10-038-407-28
; Sequence 28, Application US/10038407
; Publication No. US20030105282A1
; GENERAL INFORMATION:
; APPLICANT: Pinter, Abraham
; TITLE OF INVENTION: HIV-1 gp120 V1/V2 DOMAIN EPITOPES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/18679
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-28
```

```
Query Match 77.8%; Score 35; DB 14; Length 365;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 FYSLKIVPI 9
Db 335 FYKLDIVPI 343
```

```
RESULT 20
US-10-866-527-24
; Sequence 24, Application US/10866527
; Publication No. US20050025779A1
; GENERAL INFORMATION:
; APPLICANT: VaxGen, Inc.
; APPLICANT: Berman, Phillip W
; APPLICANT: Jobs, David V
; TITLE OF INVENTION: HIV-1 ENVELOPE GLYCOPROTEINS HAVING UNUSUAL DISULFIDE STRUCTURE
```

```
; FILE REFERENCE: 409J-000210US
; CURRENT APPLICATION NUMBER: US/10/866,527
; CURRENT FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-866-527-24
```

```
Query Match 77.8%; Score 35; DB 17; Length 468;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 FYSLKIVPI 9
Db 141 FYALDVIPI 149
```

```
RESULT 21
US-10-866-527-2
; Sequence 2, Application US/10866527
; Publication No. US20050025779A1
; GENERAL INFORMATION:
; APPLICANT: VaxGen, Inc.
; APPLICANT: Berman, Phillip W
; APPLICANT: Jobs, David V
; TITLE OF INVENTION: HIV-1 ENVELOPE GLYCOPROTEINS HAVING UNUSUAL DISULFIDE STRUCTURE
; FILE REFERENCE: 409J-000210US
; CURRENT APPLICATION NUMBER: US/10/866,527
; CURRENT FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-866-527-2
```

```
Query Match 77.8%; Score 35; DB 17; Length 484;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 FYSLKIVPI 9
Db 152 FYKLDIVPI 160
```

```
RESULT 22
US-10-866-527-102
; Sequence 102, Application US/10866527
; Publication No. US20050025779A1
; GENERAL INFORMATION:
; APPLICANT: VaxGen, Inc.
; APPLICANT: Berman, Phillip W
; APPLICANT: Jobs, David V
; TITLE OF INVENTION: HIV-1 ENVELOPE GLYCOPROTEINS HAVING UNUSUAL DISULFIDE STRUCTURE
; FILE REFERENCE: 409J-000210US
; CURRENT APPLICATION NUMBER: US/10/866,527
; CURRENT FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 102
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-866-527-102
```

```
Query Match 77.8%; Score 35; DB 17; Length 486;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1 FYSLKIVPI 9
Db      155 FYKLDIVPI 163

RESULT 23
US-10-866-527-72
; Sequence 72, Application US/10866527
; Publication No. US20050025779A1
; GENERAL INFORMATION:
; APPLICANT: VaxGen, Inc.
; APPLICANT: Berman, Phillip W
; APPLICANT: Jobses, David V
; TITLE OF INVENTION: HIV-1 ENVELOPE GLYCOPROTEINS HAVING UNUSUAL DISULFIDE STRUCTURE
; FILE REFERENCE: 4093-000210US
; CURRENT APPLICATION NUMBER: US/10/866,527
; CURRENT FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-866-527-72

Query Match      77.8%; Score 35; DB 17; Length 488;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 FYSLKIVPI 9
Db      147 FYKLDIVPI 155

RESULT 24
US-10-866-527-56
; Sequence 56, Application US/10866527
; Publication No. US20050025779A1
; GENERAL INFORMATION:
; APPLICANT: VaxGen, Inc.
; APPLICANT: Berman, Phillip W
; APPLICANT: Jobses, David V
; TITLE OF INVENTION: HIV-1 ENVELOPE GLYCOPROTEINS HAVING UNUSUAL DISULFIDE STRUCTURE
; FILE REFERENCE: 4093-000210US
; CURRENT APPLICATION NUMBER: US/10/866,527
; CURRENT FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-866-527-56

Query Match      77.8%; Score 35; DB 17; Length 490;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 FYSLKIVPI 9
Db      151 FYKLDIVPI 159

RESULT 25
US-10-371-472-19
; Sequence 19, Application US/10371472
; Publication No. US20040052821A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/10/371,472
; CURRENT FILING DATE: 2003-02-21
```

```
; PRIOR APPLICATION NUMBER: US/09/419,362
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 494
; TYPE: PRT
; ORGANISM: HIV
US-10-371-472-19

Query Match      77.8%; Score 35; DB 15; Length 494;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 FYSLKIVPI 9
Db      145 FYKLDIVPI 153

RESULT 26
US-10-371-472-25
; Sequence 25, Application US/10371472
; Publication No. US20040052821A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/10/371,472
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/419,362
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 495
; TYPE: PRT
; ORGANISM: HIV
US-10-371-472-25

Query Match      77.8%; Score 35; DB 15; Length 495;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 FYSLKIVPI 9
Db      152 FYKLDIVPI 160

RESULT 27
US-10-371-472-28
; Sequence 28, Application US/10371472
; Publication No. US20040052821A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/10/371,472
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/419,362
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
```

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 495
; TYPE: PRT
; ORGANISM: HIV
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(495)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-371-472-28

Query Match 77.8%; Score 35; DB 15; Length 495;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 152 FYKLDIVPI 160

RESULT 28
US-09-759-841-4
; Sequence 4, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
; APPLICANT: Rickett, Graham A
; APPLICANT: Dobbs, Susan
; APPLICANT: Perros, Mancusos
; TITLE OF INVENTION: Assay Method
; FILE REFERENCE: PC10348APME
; CURRENT APPLICATION NUMBER: US/09/759,841
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: GB 0000661.9
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000663.5
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000659.3
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-759-841-4

Query Match 77.8%; Score 35; DB 9; Length 503;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 173 FYELDIVPI 181

RESULT 29
US-10-866-527-114
; Sequence 114, Application US/10866527
; Publication No. US20050025779A1
; GENERAL INFORMATION:
; APPLICANT: VaxGen, Inc.
; APPLICANT: Berntan, Phillip W
; APPLICANT: Jobses, David V
; TITLE OF INVENTION: HIV-1 ENVELOPE GLYCOPROTEINS HAVING UNUSUAL DISULFIDE STRUCTURE
; FILE REFERENCE: 409J-000210US
; CURRENT APPLICATION NUMBER: US/10/866,527
; CURRENT FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1

US-10-866-527-114

Query Match 77.8%; Score 35; DB 17; Length 509;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 151 FYKLDIVPI 159

RESULT 30
US-10-866-527-94
; Sequence 94, Application US/10866527
; Publication No. US20050025779A1
; GENERAL INFORMATION:
; APPLICANT: VaxGen, Inc.
; APPLICANT: Berntan, Phillip W
; APPLICANT: Jobses, David V
; TITLE OF INVENTION: HIV-1 ENVELOPE GLYCOPROTEINS HAVING UNUSUAL DISULFIDE STRUCTURE
; FILE REFERENCE: 409J-000210US
; CURRENT APPLICATION NUMBER: US/10/866,527
; CURRENT FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 94
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-866-527-94

Query Match 77.8%; Score 35; DB 17; Length 511;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 152 FYKLDIVPI 160

RESULT 31
US-10-462-040A-49
; Sequence 49, Application US/10462040A
; Publication No. US20040106105A1
; GENERAL INFORMATION:
; APPLICANT: TORAN GARCIA, JOSE LUIS
; APPLICANT: MARTINEZ ALONSO, CARLOS
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: 621032-8/JP/B-5129
; CURRENT APPLICATION NUMBER: US/10/462,040A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: EP 02380126.9
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus type 1
US-10-462-040A-49

Query Match 77.8%; Score 35; DB 16; Length 515;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 184 FYKLDIVPI 192

RESULT 32
US-10-462-040A-45
; Sequence 45, Application US/10462040A


```
; Publication No. US20040106105A1
; GENERAL INFORMATION:
; APPLICANT: TORAN GARCIA, JOSE LUIS
; APPLICANT: MARTINEZ ALONSO, CARLOS
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: 621032-8/JP/B-5129
; CURRENT APPLICATION NUMBER: US/10/462,040A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: EP 02380126.9
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus type 1
US-10-462-040A-45

Query Match      77.8%; Score 35; DB 16; Length 518;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 184 FVKLDIVPI 192

RESULT 33
US-10-462-040A-46
; Sequence 46, Application US/10462040A
; Publication No. US20040106105A1
; GENERAL INFORMATION:
; APPLICANT: TORAN GARCIA, JOSE LUIS
; APPLICANT: MARTINEZ ALONSO, CARLOS
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: 621032-8/JP/B-5129
; CURRENT APPLICATION NUMBER: US/10/462,040A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: EP 02380126.9
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus type 1
US-10-462-040A-46

Query Match      77.8%; Score 35; DB 16; Length 518;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 184 FVKLDIVPI 192

RESULT 34
US-10-462-040A-47
; Sequence 47, Application US/10462040A
; Publication No. US20040106105A1
; GENERAL INFORMATION:
; APPLICANT: TORAN GARCIA, JOSE LUIS
; APPLICANT: MARTINEZ ALONSO, CARLOS
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: 621032-8/JP/B-5129
; CURRENT APPLICATION NUMBER: US/10/462,040A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: EP 02380126.9
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47

Query Match      77.8%; Score 35; DB 16; Length 518;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 184 FVKLDIVPI 192

RESULT 35
US-10-462-040A-48
; Sequence 48, Application US/10462040A
; Publication No. US20040106105A1
; GENERAL INFORMATION:
; APPLICANT: TORAN GARCIA, JOSE LUIS
; APPLICANT: MARTINEZ ALONSO, CARLOS
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: 621032-8/JP/B-5129
; CURRENT APPLICATION NUMBER: US/10/462,040A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: EP 02380126.9
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus type 1
US-10-462-040A-48

Query Match      77.8%; Score 35; DB 16; Length 518;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
Db 184 FVKLDIVPI 192

RESULT 36
US-10-335-394-50
; Sequence 50, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/10/335,394
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 587
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-50

Query Match      77.8%; Score 35; DB 14; Length 587;
Best Local Similarity 77.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 1 FYSLKIVPI 9
|||
Db 248 FYKLDIVPI 256

RESULT 37
US-10-335-394-56
; Sequence 56, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/10/335,394
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-56

Query Match 77.8%; Score 35; DB 14; Length 595;
Best Local Similarity 77.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
|||
Db 256 FYKLDIVPI 264

RESULT 38
US-10-335-394-52
; Sequence 52, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/10/335,394
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-52

Query Match 77.8%; Score 35; DB 14; Length 601;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
|||

Db 262 FYKLDIVPI 270

RESULT 39
US-09-254-783A-1
; Sequence 1, Application US/09254783A
; Patent No. US20020035734A1
; GENERAL INFORMATION:
; APPLICANT: Boeynaems, Jeanmarie
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: G Protein Coupled Receptor Showing Selective Affinity for ATP
; FILE REFERENCE: 9409/2062
; CURRENT APPLICATION NUMBER: US/09/254,783A
; CURRENT FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: PCT/BE98/00108
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: EP97870101.9
; PRIOR FILING DATE: 1997-07-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 795
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-254-783A-1

Query Match 77.8%; Score 35; DB 9; Length 795;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLKIVPI 9
|||
Db 197 YSIKVPV 204

RESULT 40
US-10-152-058-1
; Sequence 1, Application US/10152058
; Publication No. US20020142988A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; APPLICANT: Boeynaems, Jeanmarie
; TITLE OF INVENTION: G Protein Coupled Receptor Showing Selective Affinity for ATP
; FILE REFERENCE: 9409/2062
; CURRENT APPLICATION NUMBER: US/10/152,058
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: PCT/BE98/00108
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: EP97870101.9
; PRIOR FILING DATE: 1997-07-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 795
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-152-058-1

Query Match 77.8%; Score 35; DB 13; Length 795;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLKIVPI 9
|||
Db 197 YSIKVPV 204

Search completed: February 24, 2005, 19:27:11
Job time : 132 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: February 24, 2005, 19:03:44 ; Search time 39 Seconds

(without alignments)
22,204 Million cell updates/sec

Title: US-09-914-205-5

Perfect score: 45

Sequence: 1 FYSLKIVPI 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	82.2	301	2 T24651	hypothetical prote
2	37	82.2	383	2 AB2808	hypothetical prote
3	37	82.2	383	2 H97586	probable sulfonate
4	37	82.2	1000	2 F70368	cation efflux (Acr
5	36	80.0	115	2 T07576	hypothetical prote
6	36	80.0	253	2 D70166	pnp protein (pnp
7	36	80.0	452	1 S29510	ubiquinol-cytochro
8	36	80.0	453	1 A32629	ubiquinol-cytochro
9	36	80.0	453	1 ZPBOC2	ubiquinol-cytochro
10	36	80.0	2054	2 T07584	hypothetical prote
11	35	77.8	211	2 S25938	env protein - huma
12	35	77.8	219	2 S25939	env protein - huma
13	35	77.8	245	2 F81162	ubiquinone/menaqui
14	35	77.8	473	2 JC7359	splicing factor, S
15	35	77.8	506	2 A40218	envelop glycoprote
16	35	77.8	553	2 G90593	subtilisin, serine
17	35	77.8	843	1 H44001	env polyprotein pr
18	35	77.8	846	1 VCLJND	env polyprotein pr
19	35	77.8	852	1 VCLJBR	env polyprotein -
20	35	77.8	854	2 S13288	env protein - huma
21	34	75.6	218	2 G72754	probable phosphoen
22	34	75.6	526	2 D71805	protein-export mem
23	34	75.6	591	2 A99444	acylaminoacyl-pept
24	34	75.6	729	1 VCLJJK	env polyprotein pr
25	34	75.6	847	2 T09448	envelope glycoprot
26	34	75.6	847	2 S13289	env protein - huma
27	34	75.6	851	2 S33985	env polyprotein -
28	34	75.6	852	2 T12016	envelope glycoprot
29	34	75.6	853	2 S54384	envelope glycoprote

30	34	75.6	855	1 VCLJZR	env polyprotein pr
31	34	75.6	856	1 A44963	env polyprotein pr
32	34	75.6	856	1 VCLJ3W	env polyprotein pr
33	34	75.6	856	1 VCLJH3	env polyprotein pr
34	34	75.6	856	1 VCLJVL	env polyprotein pr
35	34	75.6	861	1 VCLJSC	env polyprotein pr
36	34	75.6	861	1 VCLJKB	env polyprotein pr
37	34	75.6	861	1 VCLJLV	env polyprotein pr
38	34	75.6	1882	1 GNVVTR	genome polyprotein
39	33	73.3	82	2 T17870	hypothetical prote
40	33	73.3	253	2 B87667	ABC-2 type transpo
41	33	73.3	259	2 F82707	conserved hypothet
42	33	73.3	347	2 T21067	hypothetical prote
43	33	73.3	399	2 S54644	translation initia
44	33	73.3	437	2 C72600	hypothetical prote
45	33	73.3	454	2 H83773	transcription regu

ALIGNMENTS

RESULT 1

T24651

hypothetical protein T07C5.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T24651

R:McMurray, A.

submitted to the EMBL Data Library, July 1995

A:Reference number: Z19917

A:Accession: T24651

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-301 <WIL>

A:Cross-references: UNIPROT:Q22299; EMBL:Z50006; PIDN:CAA90300.1; GSPDB:GN00028; CESP:T07C5

A:Experimental source: clone T07C5

C:Genetics:

A:Gene: CESP:T07C5.4

A:Map position: X

A:Introns: 20/3; 223/1

Query Match 82.2%; Score 37; DB 2; Length 301;

Best Local Similarity 77.8%; Pred. No. 6.4;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9

Db 103 YYSTKIVPI 111

RESULT 2

AB2808

hypothetical protein ssuA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens

C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C:Accession: AB2808

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan

i Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AB2808

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-383 <KUR>

A:Cross-references: UNIPROT:Q8UE77; GB:AE008688; PIDN:AAL42880.1; PID:g17740332; GSPDB:G

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: ssuA

A:Map position: circular chromosome

Query Match 82.2%; Score 37; DB 2; Length 383;
Best Local Similarity 87.5%; Pred. No. 8.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVP 8
|||:||||
Db 361 FYDLKIVP 368

RESULT 3
H97586
probable sulfonate binding protein precursor (AF075709) [imported] - Agrobacterium tumefaciens
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: H97586
A: Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: H97586
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-383 <KUR>
A:Cross-references: UNIPROT:Q8UE77; GB:AE007869; PIDN:AAK87649.1; PID:g15157002; GSPDB:C
C:Genetics:
A:Gene: AGR_C_3458
A:Map position: circular chromosome

Query Match 82.2%; Score 37; DB 2; Length 383;
Best Local Similarity 87.5%; Pred. No. 8.2;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVP 8
|||:||||
Db 361 FYDLKIVP 368

RESULT 4
F70368
cation efflux (AcrB/AcrD/AcrF family) - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: F70368
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196866; PMID:9537320
A:Accession: F70368
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1000 <AOF>
A:Cross-references: UNIPROT:Q66977; GB:AE000707; NID:G2983342; PIDN:AA06934.1; PID:g2983342
A:Experimental source: strain VF5
C:Genetics:
A:Gene: acrB4
C:Superfamily: acriflavin resistance protein

Query Match 82.2%; Score 37; DB 2; Length 1000;
Best Local Similarity 87.5%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLKIVPI 9
|||:||||
Db 25 YSLKIVPI 32

RESULT 5
T07576
hypothetical protein 115 - Japanese black pine chloroplast
C:Species: chloroplast Pinus thunbergiana (Japanese black pine)

C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C:Accession: T07576
R:Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiyura, M. Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994
A:Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome
A:Reference number: Z16030; MUID:95024047; PMID:7937893
A:Accession: T07576
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-115 <WAK>
A:Cross-references: UNIPROT:Q33000; EMBL:D17510; NID:g529643; PIDN:BAA04452.1; PID:g1262;
C:Genetics:
A:Genome: chloroplast
C:Keywords: chloroplast

Query Match 80.0%; Score 36; DB 2; Length 115;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
|||:||||
Db 7 FYSIKLPPI 15

RESULT 6
D70166
pHNP protein (pHNP) homolog - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: D70166
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lachigra, R.; White, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: D70166
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-253 <KLE>
A:Cross-references: UNIPROT:O51483; GB:AE001155; GB:AE000783; NID:g2688448; PIDN:AA06690;
A:Experimental source: strain E31
C:Superfamily: ATP-binding protein PhnP (PhnP)

Query Match 80.0%; Score 36; DB 2; Length 253;
Best Local Similarity 88.9%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
|||:||||
Db 141 FKSLKIVPI 149

RESULT 7
S29510
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II precursor - rat
N:Alternate names: cytochrome bc1 complex core protein II
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1993 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C:Accession: S29510
R:Hosokawa, Y.; Suzuki, H.; Toda, H.; Nishikimi, M.; Ozawa, T. Biochem. Int. 20, 731-737, 1990
A:Title: The primary structure of the precursor to core protein II, a putative member of ce analysis.
A:Reference number: S29510; MUID:90282728; PMID:2162168
A:Accession: S29510
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-452 <HOS>
A:Cross-references: UNIPROT:P32551
C:Genetics:
A:Genome: nuclear

C:Superfamily: mitochondrial processing peptidase alpha chain
C:Keywords: mitochondrial matrix; mitochondrion; oxidative phosphorylation; oxidoreducta
F:1-14/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:15-452/Product: ubiquinol-cytochrome-c reductase core protein II #status predicted <MA

Query Match 80.0%; Score 36; DB 1; Length 452;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVP 8
DB 13 FYSLKVAP 20

RESULT 8
A32629
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II precursor - human
C:Species: Homo sapiens (man)
C:Date: 21-May-1990 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C:Accession: A32629
R:Hosokawa, Y.; Suzuki, H.; Toda, H.; Nishikimi, M.; Ozawa, T.
J. Biol. Chem. 264, 13483-13488, 1989
A:Title: Complementary DNA encoding core protein II of human mitochondrial cytochrome b
A:Reference number: A32629; MUID:89340421; PMID:2547763
A:Accession: A32629
A:Molecule type: mRNA
A:Residues: 1-453 <HOS>
A:Cross-references: UNIPROT:P22695; GB:J04973; NID:G180927; PIDN:AAA35710.1; PID:G180928
A:Note: the authors translated the codon AGA for residue 360 as Thr
C:Genetics:
A:Gene: GDB:UQCRC2
A:Cross-references: GDB:141851; OMIM:191329
A:Map position: 16p12.3-16p12.3
C:Superfamily: mitochondrial processing peptidase alpha chain
C:Keywords: hydrolase; mitochondrial matrix; mitochondrion; oxidative phosphorylation; o
F:1-14/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:15-453/Product: ubiquinol-cytochrome-c reductase core protein II #status predicted <MA

Query Match 80.0%; Score 36; DB 1; Length 453;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVP 8
DB 13 FYSLKVAP 20

RESULT 9
ZFBOC2
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C:Accession: S16221; S14093
R:Gencic, S.; Schaeffer, H.; von Jagow, G.
Eur. J. Biochem. 199, 123-131, 1991
A:Title: Core I protein of bovine ubiquinol-cytochrome-c reductase; an additional member
re of the proteins.
A:Reference number: S16220; MUID:91293112; PMID:1712295
A:Accession: S16221
A:Molecule type: mRNA
A:Residues: 1-453 <GEN>
A:Cross-references: UNIPROT:P23004; GB:X59693; NID:G299; PIDN:CAA42214.1; PID:G300
A:Note: part of this sequence, including the amino end of the mature protein, was confir
R:Cocco, T.; Lorusso, M.; Sardanelli, A.M.; Minuto, M.; Ronchi, S.; Tedeschi, G.; Papa,
Eur. J. Biochem. 195, 731-734, 1991
A:Title: Structural and functional characteristics of polypeptide subunits of the bovine
A:Reference number: S14093; MUID:91153313; PMID:1847870
A:Accession: S14093
A:Molecule type: protein
A:Residues: 'T', 16-40, 'R', 42-46 <COC>
C:Superfamily: mitochondrial processing peptidase alpha chain
C:Keywords: hydrolase; mitochondrial matrix; mitochondrion; oxidative phosphorylation; c
F:1-14/Domain: transit peptide (mitochondrion) #status predicted <TNP>

F:15-453/Product: ubiquinol-cytochrome-c reductase core protein II #status experimental <
C:Superfamily: mitochondrial processing peptidase alpha chain
C:Keywords: mitochondrial matrix; mitochondrion; oxidative phosphorylation; oxidoreducta
F:1-14/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:15-452/Product: ubiquinol-cytochrome-c reductase core protein II #status predicted <MA

Query Match 80.0%; Score 36; DB 1; Length 453;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVP 8
DB 13 FYSLKVAP 20

RESULT 10
T07584
hypochemical protein 2054 - Japanese black pine chloroplast
C:Species: chloroplast Pinus thunbergiana (Japanese black pine)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C:Accession: T07584
R:Wakasugi, T.; Taudzuki, J.; Ito, S.; Nakashima, K.; Taudzuki, T.; Sugiyura, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994
A:Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome
A:Reference number: Z16030; MUID:95024047; PMID:7937893
A:Accession: T07584
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2054 <WAK>
A:Cross-references: UNIPROT:P41653; EMBL:D17510; NID:G529643; PIDN:BAA04460.1; PID:G1262;
C:Genetics:
A:Gene: chloroplast
C:Keywords: chloroplast

Query Match 80.0%; Score 36; DB 2; Length 2054;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
DB 97 FYSLKIVPI 105

RESULT 11
S25938
env protein - human immunodeficiency virus type 1 (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 25-Feb-1994 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
C:Accession: S25938
R:Guo, H.G.; Chermann, J.C.; Waters, D.; Hall, L.; Louie, A.; Gallo, R.C.; Streicher, H.;
Nature 349, 745-746, 1991
A:Title: Sequence analysis of original HIV-1.
A:Reference number: S25937; MUID:91156044; PMID:2000145
A:Accession: S25938
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-211 <GUO>
A:Cross-references: UNIPROT:Q79141; EMBL:X57446; NID:G60204; PIDN:CAA40692.1; PID:G60205
A:Experimental source: strain JBB
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1991
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein

Query Match 77.8%; Score 35; DB 2; Length 211;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
DB 134 FYKLDIVPI 142

RESULT 12
S25939
env protein - human immunodeficiency virus type 1 (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 25-Feb-1994 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
C:Accession: S25939
R:Guo, H.G.; Chermann, J.C.; Waters, D.; Hall, L.; Louie, A.; Gallo, R.C.; Streicher, H.
Nature 349, 745-746, 1991
A>Title: Sequence analysis of original HIV-1.
A:Reference number: S25937; MUID:91156044; PMID:2000145
A:Accession: S25939
A:Molecule type: DNA
A:Residues: 1-219 <GUO>
A:Cross-references: UNIPROT:Q79144; EMBL:X57447; NID:960212; PIDN:CAA406
A:Experimental source: strain JBB
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1991
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: Coat protein

Query Match 77.8%; Score 35; DB 2; Length 219;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
||| |||||
Db 134 FYKLDIVPI 142

RESULT 13
F81162
ubiquinone/menaquinone biosynthesis methyltransferase UbiE NMB0743 [imported] - Neisseri
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: F81162
R:Tetrelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A>Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: F81162
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-245 <TET>
A:Cross-references: UNIPROT:Q9K075; GB:AE002429; GB:AE002098; NID:G7225969; PIDN:AAF4115
A:Experimental source: serogroup B, strain MCS8
C:Genetics:
A:Gene: NMB0743
C:Superfamily: spore germination protein C2; bioC homology

Query Match 77.8%; Score 35; DB 2; Length 245;
Best Local Similarity 55.6%; Pred. No. 14;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
||| |||||
Db 179 FYSFLLPV 187

RESULT 14
JC7359
splicing factor, Ssf-1 - human
C:Species: Homo sapiens (man)
C>Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C:Accession: JC7359
R:Suarez-Huerta, N.; Boeynaems, J.M.; Communi, D.
Biochem. Biophys. Res. Commun. 275, 37-42, 2000
A>Title: Cloning, genomic organization, and tissue distribution of human Ssf-1.
A:Reference number: JC7359
A:Contents: Placenta
A:Accession: JC7359
A:Molecule type: mRNA

A:Residues: 1-473 <SUA>
A:Cross-references: UNIPROT:Q9NQ55; GB:AJ292529
C:Comment: This factor, involved in the second step of mRNA splicing, is a negative regul
C:Genetics:
A:Gene: Ssf-1
A:Map position: 19p31
C:Keywords: neutrophil; placenta

Query Match 77.8%; Score 35; DB 2; Length 473;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLKIVPI 9
||| |||||
Db 197 YSIKVPV 204

RESULT 15
A40218
envelop glycoprotein gp120 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A40218
R:Turner, S.; Fizard, R.; DeMarinis, J.; Pepinsky, R.B.; Zullo, J.; Schooley, R.; Fisher,
Proc. Natl. Acad. Sci. U.S.A. 89, 1335-1339, 1992
A>Title: Resistance of primary isolates of human immunodeficiency virus type 1 to neutral
A:Reference number: A40218; MUID:92159044; PMID:1741386
A:Accession: A40218
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-506 <TUR>
A:Cross-references: UNIPROT:Q9PY23
A:Experimental source: isolate p17
A:Note: sequence extracted from NCBI backbone (NCBI:82240)
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: glycoprotein

Query Match 77.8%; Score 35; DB 2; Length 506;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
||| |||||
Db 172 FYKLDIVPI 180

RESULT 16
G90593
subtilisin, serine proteinase [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: G90593
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A>Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: G90593
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-553 <KUR>
A:Cross-references: UNIPROT:Q98PR4; GB:AL445566; PID:gl4090070; PIDN:CAC13828.1; GSPDB:GN
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPV 6550
A:Genetic code: SGC3

Query Match 77.8%; Score 35; DB 2; Length 553;
Best Local Similarity 77.8%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
||| |||||
Db 117 FYSLNIPPI 125

```
RESULT 17
H44001
env polyprotein precursor - human immunodeficiency virus type 1 (strain YU-2)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: H44001
R:Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6600, 1992
A:Title: Complete nucleotide sequence, genome organization, and biological properties of
A:Reference number: A44001; MUID:93021387; PMID:1404605
A:Accession: H44001
A:Molecule type: DNA
A:Residues: 1-843 <L1Y>
A:Cross-references: UNIPROT:P35961; GB:M93258
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:19-35/Region: hydrophobic
F:30-489/Product: coat protein gp120 #status predicted <GP1>
F:490-843/Product: coat protein gp41 #status predicted <GP2>
F:499-515/Region: hydrophobic
F:673-689/Region: hydrophobic
F:738-755/Domain: transmembrane #status predicted <TMN>
F:87.129,135,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,435
Query Match 77.8%; Score 35; DB 1; Length 843;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
DB 174 FVSLDIVPI 182

RESULT 18
VCLJND
env polyprotein precursor - human immunodeficiency virus type 1 (isolate NDK)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: JQ0066
R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;
Gene 81, 275-284, 1989
A:Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human immun
A:Reference number: JQ0065; MUID:90034200; PMID:2806917
A:Accession: JQ0066
A:Molecule type: DNA
A:Residues: 1-846 <SPI>
A:Cross-references: UNIPROT:P18799; GB:M27323; NID:G328154; PIDN:AAA44873.1; PID:G328162
A:Note: the authors translated the codon GCG for residue 523 as Arg
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <CP1>
F:502-846/Product: coat protein gp41 #status predicted <CP2>
F:502-520/Domain: transmembrane #status predicted <TM1>
F:674-692/Domain: transmembrane #status predicted <TM2>
F:87.129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,608
Query Match 77.8%; Score 35; DB 1; Length 846;
Best Local Similarity 77.8%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 FVSLKIVPI 9
DB 167 FYKLDIVPI 175

RESULT 19
VCLJBR
env polyprotein - human immunodeficiency virus type 1 (isolate BR)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C:Accession: A31667
R:Anand, R.; Thayer, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar, S.;
Virolgy 168, 79-89, 1989
A:Title: Biological and molecular characterization of human immunodeficiency virus (HIV-1)
A:Reference number: A94389; MUID:89085613; PMID:2789516
A:Accession: A31667
A:Molecule type: DNA
A:Residues: 1-852 <ANA>
A:Cross-references: UNIPROT:P12488
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: capsid protein; coat protein; polyprotein; transmembrane protein
F:1-516/Product: coat protein gp120 #status predicted <CP1>
F:517-852/Product: coat protein gp41 #status predicted <CP2>
Query Match 77.8%; Score 35; DB 1; Length 852;
Best Local Similarity 77.8%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
DB 174 FYKLDIVPI 182

RESULT 20
SI3288
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: SI3288
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Digne, A.; Idler, K.; Zack, J.A.;
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120 c
A:Reference number: SI3288; MUID:91043044; PMID:2172833
A:Accession: SI3288
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-854 <OBR>
A:Cross-references: UNIPROT:Q85582; UNIPROT:Q72502; UNIPROT:Q90178; UNIPROT:Q78243; UNIP
C:Superfamily: type E retrovirus env polyprotein
Query Match 77.8%; Score 35; DB 2; Length 854;
Best Local Similarity 77.8%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
DB 176 FYKLDIVPI 184

RESULT 21
G72754
probable phosphoenolpyruvate synthase APE0028 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: G72754
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
```

A:Reference number: A72450; MUID:99110339; PMID:10382966

A:Accession: G72754

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-218 <KAW>

A:Cross-references: UNIPROT:O9YGV73; DBJ:AP000058; NID:95103388; PIDN:BAA78937.1; PID:dl

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE0028

Query Match

Best Local Similarity 75.6%; Score 34; DB 2; Length 218;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FYSLKIVP 8

DB 21 FYAMKLVP 28

RESULT 22

D71805

protein-export membrane protein - Helicobacter pylori (strain J99)

C:Species: Helicobacter pylori

A:Variety: strain J99

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C:Accession: D71805

R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path

A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: D71805

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-526 <ARN>

A:Cross-references: UNIPROT:Q9ZJ66; GB:AE001567; GB:AE001439; NID:94156065; PIDN:AAD0702

A:Experimental source: strain J99

C:Genetics:

A:Gene: secD

C:Superfamily: protein export membrane protein secD

Query Match

Best Local Similarity 75.6%; Score 34; DB 2; Length 526;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9

DB 122 FYSVKLTPL 130

RESULT 23

A99444

acylaminoacyl-peptidase, probable (apeH-3) [imported] - Sulfolobus solfataricus

C:Species: Sulfolobus solfataricus

C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C:Accession: A99444

R:She, Q.; Jing, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-

Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Rgoc, H.P.; Redder, E.

arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A99139

A:Accession: A99444

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-591 <KUR>

A:Cross-references: UNIPROT:Q97VD6; GB:AE006641; NID:913816011; PIDN:AAK42808.1; GSPDB:C

C:Genetics:

A:Gene: apeH-3

Query Match

Best Local Similarity 75.6%; Score 34; DB 2; Length 591;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FYSLKIVP 8

DB 7 YYSIKLVP 14

RESULT 24

VCLJKX

env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)

N:Alternate names: coat polyprotein

N:Contains: coat protein gp120; coat protein gp32

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Mar-1996

C:Accession: B42995

R:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.

Virolgy 189, 534-546, 1992

A:Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated t

A:Reference number: A42995; MUID:92351552; PMID:1322587

A:Accession: B42995

A:Molecule type: mRNA

A:Residues: 1-729 <SHI>

A:Cross-references: GB:S41266; GB:D01206

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F:1-689/Domain: extracellular #status predicted <EXT>

F:1-33/Domain: signal sequence #status predicted <SIG>

F:17-33/Region: hydrophobic #status predicted

F:34-517/Product: coat protein gp120 #status predicted <CP1>

F:514-517/Region: cleavage processing #status predicted

F:518-729/Product: coat protein gp32 #status predicted <CP2>

F:518-534/Region: hydrophobic #status predicted

F:690-711/Domain: transmembrane #status predicted <TM1>

F:712-729/Domain: intracellular #status predicted <INT>

F:93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414,

Query Match 75.6%; Score 34; DB 1; Length 729;

Best Local Similarity 66.7%; Pred. No. 65;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9

DB 179 FYKLDVVPI 187

RESULT 25

T09448

envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C:Accession: T09448

R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,

submitted to the EMBL Data Library, July 1996

A:Reference number: Z16673

A:Accession: T09448

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-847 <PAN>

A:Cross-references: UNIPROT:Q75760; EMBL:U63632; NID:91465777; PID:91465781

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

Query Match

Best Local Similarity 75.6%; Score 34; DB 2; Length 847;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9

DB 173 FYKLDVVPI 181


```
RESULT 26
S13289
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S13289
R:O'Brien, W.A.; Kovanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A:Reference number: S13288; MUID:91043044; PMID:2172833
A:Accession: S13289
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-847 <OBR>
A:Cross-references: UNIPROT:Q75760
C:Superfamily: type E retrovirus env polyprotein

Query Match          75.6%; Score 34; DB 2; Length 847;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
   |||:|
Db 173 FYKLDVPI 181

RESULT 27
S33985
env polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S33985
R:Carlini, F.
submitted to the EMBL Data Library, November 1991
A:Reference number: S33979
A:Accession: S33985
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-851 <CAR>
A:Cross-references: UNIPROT:Q78243; EMBL:Z11530; NID:G60192; PIDN:CAA77628.1; PID:G60199
C:Superfamily: type E retrovirus env polyprotein

Query Match          75.6%; Score 34; DB 2; Length 851;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
   |||:|
Db 176 FYKLDIPI 184

RESULT 28
T12016
envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T12016
R:McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
AIDS Res. Hum. Retroviruses 14, 329-337, 1998
A:Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S
A:Reference number: T17379; MUID:98178716; PMID:9519894
A:Accession: T12016
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-852 <MCC>
A:Cross-references: UNIPROT:O41883; EMBL:U90934; NID:G2351783; PIDN:AAC59271.1; PID:G235
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein

Query Match          75.6%; Score 34; DB 2; Length 852;
Best Local Similarity 66.7%; Pred. No. 76;
```

```
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
   |||:|
Db 175 FYKLDVPI 183

RESULT 29
S54384
envelope polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S54384
R:Theodore, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A:Reference number: S54377
A:Accession: S54384
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-853 <THE>
A:Cross-references: UNIPROT:P12487; EMBL:M22639; NID:G329377; PIDN:AAA45370.1; PID:G32937
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: polyprotein

Query Match          75.6%; Score 34; DB 2; Length 853;
Best Local Similarity 77.8%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
   |||:|
Db 173 FYRLDIVPI 181

RESULT 30
VCLJZR
env polyprotein precursor - human immunodeficiency virus Zr-6
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus Zr-6
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: D26192
R:Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu
Gene 52, 71-82, 1987
A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleotic
A:Reference number: A26192; MUID:87248097; PMID:3036660
A:Accession: D26192
A:Molecule type: DNA
A:Residues: 1-855 <SRI>
A:Cross-references: UNIPROT:P04580; GB:K03458; GB:M16322; NID:G329398; PIDN:AAA45380.1; I
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-855/Product: env polyprotein #status predicted <MAT>
F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>
F:501-855/Product: transmembrane glycoprotein #status predicted <TM>
F:87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404,

Query Match          75.6%; Score 34; DB 1; Length 855;
Best Local Similarity 77.8%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
   |||:|
Db 174 FYRLDIVPI 182

RESULT 31
A44963
env polyprotein precursor - human immunodeficiency virus type 1 (isolate Z321)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
```

A:Note: host Homo sapiens (man)
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C:Accession: A44963
R:Srinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J.
AIDS Res. Hum. Retroviruses 5, 121-129, 1989
A:Title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: nu
A:Reference number: A44963; MUID:89228766; PMID:2713163
A:Accession: A44963
A:Molecule type: DNA
A:Residues: 1-856 <SRI>
A:Cross-references: UNIPROT:P05881; GB:M15896; NID:g329394.1; PID:g329394
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-520/Product: coat protein gp120 #status predicted <CP1>
F:521-856/Product: coat protein gp41 #status predicted <CP2>
F:864-705/Domain: transmembrane #status predicted <TMN>
F:87,132,138,152,156,183,198,242,263,277,294,302,339,398,402,411,448,461,462,465,611
Query Match 75.6%; Score 34; DB 1; Length 856;
Best Local Similarity 77.8%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 FYSLKIVPI 9
DB 172 FYRLDIVPI 180
RESULT 32
VCLJ3W
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C:Accession: A24774
R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.
Cell 45, 637-648, 1986
A:Title: Identification and characterization of conserved and variable regions in the en
A:Reference number: A24774; MUID:86218077; PMID:2423250
A:Accession: A24774
A:Molecule type: DNA
A:Residues: 1-856 <STA>
A:Cross-references: UNIPROT:P31872; GB:K03455; GB:M38432; NID:g1906382
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <GP1>
F:502-847/Product: coat protein gp41 #status predicted <GP2>
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459
Query Match 75.6%; Score 34; DB 1; Length 856;
Best Local Similarity 66.7%; Pred. No. 77;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 FYSLKIVPI 9
DB 171 FYRLDIVPI 179
RESULT 33
VCLJH3
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dora
nberger, J.A.; Papas, T.S.; Ghraryeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.

Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: UNIPROT:P03375; GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326;
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TMN>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 75.6%; Score 34; DB 1; Length 856;
Best Local Similarity 66.7%; Pred. No. 77;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 FYSLKIVPI 9
DB 176 FYKLDIPI 184
RESULT 34
VCLJVL
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03974
R:Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Laeky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovir
A:Reference number: A93355; MUID:85111157; PMID:2982104
A:Accession: A03974
A:Molecule type: DNA
A:Residues: 1-856 <MUE>
A:Cross-references: UNIPROT:P03376; GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TMN>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 75.6%; Score 34; DB 1; Length 856;
Best Local Similarity 66.7%; Pred. No. 77;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 FYSLKIVPI 9
DB 176 FYKLDIPI 184
RESULT 35
VCLJSC
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C:Accession: B28922
R:Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta
virology 164, 531-536, 1988
A:Title: Envelope sequences of two new United States HIV-1 isolates.
A:Reference number: A28922; MUID:88219542; PMID:3369091

A:Accession: B28922
A:Molecule type: DNA
A:Residues: 1-861 <GUR>
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-861/Product: env polyprotein #status predicted <EPD>
F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396
Query Match 75.6%; Score 34; DB 1; Length 861;
Best Local Similarity 66.7%; Pred. No. 77;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FVSLKIVPI 9
Db 177 FYKLDVPI 185

RESULT 36
VCLJRB
env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp41)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Accession: A42995
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
R:Shimizu, H.; Hasebe, F.; Teuchie, H.; Morikawa, H.; Ushijima, H.; Kitamura, T.
Virolgy 189, 534-546, 1992
A:Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated
A:Reference number: A42995; MUID:92351552; PMID:1322587
A:Accession: A42995
A:Molecule type: mRNA
A:Residues: 1-861 <SHI>
A:Cross-references: UNIPROT:P31819; GB:S41266; GB:D01206
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-689/Domain: extracellular #status predicted <EXT>
F:1-33/Domain: signal sequence #status predicted <SIG>
F:17-33/Region: hydrophobic #status predicted
F:134-517/Product: coat protein gp120 #status predicted <CP1>
F:514-517/Region: cleavage processing #status predicted
F:518-861/Product: coat protein gp41 #status predicted <CP2>
F:518-534/Region: hydrophobic #status predicted
F:690-711/Domain: transmembrane #status predicted <TM1>
F:712-861/Domain: intracellular #status predicted <INT>
F:756-772/Region: hydrophobic #status predicted
F:93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414

Query Match 75.6%; Score 34; DB 1; Length 861;
Best Local Similarity 66.7%; Pred. No. 77;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FVSLKIVPI 9
Db 179 FYKLDVPI 187

RESULT 37
VCLJLV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03975
R:Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.

A:Reference number: A90866; MUID:85099333; PMID:2981635
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <WAL>
A:Cross-references: UNIPROT:P03377; GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411,
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 75.6%; Score 34; DB 1; Length 861;
Best Local Similarity 66.7%; Pred. No. 77;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FVSLKIVPI 9
Db 181 FYKLDIPI 189

RESULT 38
GNVTR
genome polyprotein 2 - tomato ringspot virus (strain raspberry)
N:Contains: coat protein
C:Species: tomato ringspot virus
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: JQ1093
R:Rott, M.E.; Tremaine, J.H.; Rochon, D.M.
J. Gen. Virol. 72, 1505-1514, 1991
A:Title: Nucleotide sequence of tomato ringspot virus RNA-2.
A:Reference number: JQ1093; MUID:91311402; PMID:1856689
A:Accession: JQ1093
A:Molecule type: genomic RNA
A:Residues: 1-1882 <ROT>
A:Cross-references: UNIPROT:P25247; GB:D12477; GB:D01129; NID:g222674; PIDN:BA02043.1; I:
A:Note: it is uncertain whether Met-1 or Met-122 is the initiator
C:Genetics:
A:Map position: segment 2
C:Superfamily: tomato ringspot virus genome polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein
F:131-1882/Product: coat protein #status predicted <MAT>
F:269,295,1183,1316,1543,1561,1735/Binding site: carbohydrate (Asn) (covalent) #status p

Query Match 75.6%; Score 34; DB 1; Length 1882;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FVSLKIVPI 9
Db 806 FYSVKVPI 814

RESULT 39
TI7870
hypothetical protein a370R - Chlorella virus PBCV-1
C:Species: Chlorella virus PBCV-1
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: TI7870
R:Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18806
A:Accession: TI7870
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-82 <GRA>
A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96738.1
C:Genetics:
A:Note: a370R

Query Match 73.3%; Score 33; DB 2; Length 82;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YSLKIVPI 9
|.:|:|
Db 60 YALRIVPI 67

RESULT 40
B87667
ABC-2 type transporter, probable CC3372 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: B87667
R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: B87667
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-253 <STO>
A:Cross-references: UNIPROT:O9A334; GB:AB005673; NID:gl3425078; PIDN:AAK25334.1; GSPDB:G
C:Genetics: CC3372
A:Gene: CC3372
C:Superfamily: Escherichia coli probable ABC transporter yadH

Query Match 73.3%; Score 33; DB 2; Length 253;
Best Local Similarity 62.5%; Pred. No. 37;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FYSLKIVP 8
|.:|:|
Db 185 FYSIKMLP 192

Search completed: February 24, 2005, 19:15:24
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 24, 2005, 18:45:15 ; Search time 174 Seconds
(without alignments)
26.487 Million cell updates/sec

Title: US-09-914-205-5
Perfect score: 45
Sequence: 1 FVSLKIVPI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_eprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	41	91.1	772	2	Q7F8Q8	Q7F8Q8 oryza sativ
2	40	88.9	260	2	Q8D2S3	Q8D2S3 wigglewort
3	39	86.7	254	2	P88350	P88350 human immun
4	39	86.7	394	2	Q70194	Q70194 human immun
5	39	86.7	460	2	Q9WR10	Q9WR10 human immun
6	39	86.7	494	2	Q71645	Q71645 human immun
7	39	86.7	517	2	Q75603	Q75603 human immun
8	39	86.7	536	2	Q75597	Q75597 human immun
9	39	86.7	540	2	Q75601	Q75601 human immun
10	39	86.7	541	2	Q75599	Q75599 human immun
11	39	86.7	545	2	Q75598	Q75598 human immun
12	39	86.7	843	2	Q6BC09	Q6BC09 human immun
13	39	86.7	846	2	Q6XJ60	Q6XJ60 human immun
14	39	86.7	851	2	Q6HIQ0	Q6HIQ0 human immun
15	39	86.7	864	2	Q92890	Q92890 human immun
16	38	84.4	37	2	Q69722	Q69722 human immun
17	38	84.4	48	2	Q69724	Q69724 human immun
18	38	84.4	52	2	Q69720	Q69720 human immun
19	38	84.4	91	2	Q70903	Q70903 human immun
20	38	84.4	92	2	Q99C16	Q99C16 human immun
21	38	84.4	92	2	Q71257	Q71257 human immun
22	38	84.4	110	2	Q71270	Q71270 human immun
23	38	84.4	215	2	Q8JEC0	Q8JEC0 human immun
24	38	84.4	215	2	Q8Q820	Q8Q820 human immun
25	38	84.4	226	2	Q8Q813	Q8Q813 human immun
26	38	84.4	230	2	Q8Q814	Q8Q814 human immun
27	38	84.4	232	2	Q8Q831	Q8Q831 human immun
28	38	84.4	233	2	Q8JEB7	Q8JEB7 human immun
29	38	84.4	233	2	Q8JEB8	Q8JEB8 human immun
30	38	84.4	233	2	Q8Q816	Q8Q816 human immun
31	38	84.4	233	2	Q8Q819	Q8Q819 human immun

32	38	84.4	234	2	Q8Q812	Q8Q812 human immun
33	38	84.4	242	2	Q8JEB9	Q8JEB9 human immun
34	38	84.4	242	2	Q8Q832	Q8Q832 human immun
35	38	84.4	242	2	Q8Q836	Q8Q836 human immun
36	38	84.4	244	2	P88361	P88361 human immun
37	38	84.4	244	2	Q8Q818	Q8Q818 human immun
38	38	84.4	245	2	Q8Q815	Q8Q815 human immun
39	38	84.4	248	2	Q8Q827	Q8Q827 human immun
40	38	84.4	249	2	P88346	P88346 human immun
41	38	84.4	249	2	P88353	P88353 human immun
42	38	84.4	251	2	P88354	P88354 human immun
43	38	84.4	251	2	P88358	P88358 human immun
44	38	84.4	251	2	Q8Q810	Q8Q810 human immun
45	38	84.4	254	2	P88349	P88349 human immun

ALIGNMENTS

RESULT 1
Q7F8Q8
ID Q7F8Q8 PRELIMINARY; PRT; 772 AA.
AC Q7F8Q8;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Putative leucine-rich repeat transmembrane protein kinase 2.
GN Name=P0437H03.137;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP000366; BAD15408.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004674; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR plant.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00560; LRR_1; 3.
DR PRINTS; PR000019; LEURICHRPT.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
SQ ATP-binding; Kinase; Transmembrane.
KW SEQUENCE 772 AA; 84288 MW; 4EAF97FDA1A1C062 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 772;

Best Local Similarity 77.8%; Pred. No. 10;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9

Db 99 FVSLKILPV 107

RESULT 2

Q8D2S3

ID Q8D2S3 PRELIMINARY; PRT; 260 AA.

AC Q8D2S3;
DT 01-MAR-2003 (Tremblrel. 23, Created)


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DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GPI20.
DR Pfam; PF00516; GPI20; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 460
SQ SEQUENCE 460 AA; 51461 MW; FDB9643CA6056C31 CRC64;

Query Match      86.7%; Score 39; DB 2; Length 460;
Best Local Similarity 88.9%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
DB 124 FYSLDIVPI 132

RESULT 6
Q17645 PRELIMINARY; PRT; 494 AA.
AC Q71645;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95373135; PubMed=7645211;
RA Arnold C., Balfe P., Clewley J.P.;
RT "Sequence distances between env genes of HIV-1 from individuals
RT infected from the same source: implications for the investigation of
RT possible transmission events.";
RL Virology 211:198-203(1995).
DR EMBL; U23129; AAA80628.1; -.
DR HSSP; P04578; 1G9N.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GPI20.
DR Pfam; PF00516; GPI20; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 494
SQ SEQUENCE 494 AA; 55324 MW; BFCC86C039241B8F CRC64;

Query Match      86.7%; Score 39; DB 2; Length 494;
Best Local Similarity 88.9%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
DB 156 FYSLDIVPI 164

RESULT 7
Q75603 PRELIMINARY; PRT; 517 AA.
AC Q75603;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein 120 (fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96251941; PubMed=8661395; DOI=10.1006/viro.1996.0332;
RA McKeating J.A., Zhang Y.J., Arnold C., Frederiksen R., Penyo E.M.,
RA Balfe P.;
RT "Chimeric viruses expressing primary envelope glycoproteins of human
RT immunodeficiency virus type I show increased sensitivity to
RT neutralization by human sera.";
RL Virology 220:450-460(1996).
DR EMBL; U57794; AAB17032.1; -.
DR HSSP; P19549; 1MEQ.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GPI20.
DR Pfam; PF00516; GPI20; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 517
SQ SEQUENCE 517 AA; 58117 MW; 27A8C123A434800B CRC64;

Query Match      86.7%; Score 39; DB 2; Length 517;
Best Local Similarity 88.9%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
DB 183 FYSLDIVPI 191

RESULT 8
Q75597 PRELIMINARY; PRT; 536 AA.
AC Q75597;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein 120 (fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96251941; PubMed=8661395; DOI=10.1006/viro.1996.0332;
RA McKeating J.A., Zhang Y.J., Arnold C., Frederiksen R., Penyo E.M.,
RA Balfe P.;
RT "Chimeric viruses expressing primary envelope glycoproteins of human
RT immunodeficiency virus type I show increased sensitivity to
RT neutralization by human sera.";
RL Virology 220:450-460(1996).
DR EMBL; U57788; AAB17026.1; -.
DR HSSP; P19549; 1MEQ.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GPI20.
DR Pfam; PF00516; GPI20; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 536
SQ SEQUENCE 536 AA; 60052 MW; EC1FC0CDB95DE634 CRC64;

Query Match      86.7%; Score 39; DB 2; Length 536;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FYSLKIVPI 9
DB 179 FYSLDIVPI 187
```

RESULT 9
Q75601
ID Q75601 PRELIMINARY; PRT; 540 AA.
AC Q75601;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein 120 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KI4803;
RX MEDLINE=96251941; PubMed=8661395; DOI=10.1006/viro.1996.0332;
RA McKeating J.A., Zhang Y.J., Arnold C., Frederiksson R., Fenyo E.M.,
RA Balfe P.;
RT "Chimeric viruses expressing primary envelope glycoproteins of human
RT immunodeficiency virus type I show increased sensitivity to
RT neutralization by human sera.";
RL Virology 220:450-460(1996).
DR EMBL; U57792; AAB17030.1; -.
DR HSSP; P19549; 1MEQ.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
FT NON_TER 1
FT NON_TER 540
FT NON_TER 540
SQ SEQUENCE 540 AA; 60518 MW; 09BBD63ED3C247F2 CRC64;

Query Match 86.7%; Score 39; DB 2; Length 540;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 180 FVSLDIVPI 188

RESULT 10
Q75599
ID Q75599 PRELIMINARY; PRT; 541 AA.
AC Q75599;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein 120 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KI4803;
RX MEDLINE=96251941; PubMed=8661395; DOI=10.1006/viro.1996.0332;
RA McKeating J.A., Zhang Y.J., Arnold C., Frederiksson R., Fenyo E.M.,
RA Balfe P.;
RT "Chimeric viruses expressing primary envelope glycoproteins of human
RT immunodeficiency virus type I show increased sensitivity to
RT neutralization by human sera.";
RL Virology 220:450-460(1996).
DR EMBL; U57790; AAB17028.1; -.
DR HSSP; P19549; 1MEQ.

DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 541
FT NON_TER 541
SQ SEQUENCE 541 AA; 60460 MW; 7514A5AD0ABA6D37 CRC64;

Query Match 86.7%; Score 39; DB 2; Length 541;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 183 FVSLDIVPI 191

RESULT 11
Q75598
ID Q75598 PRELIMINARY; PRT; 545 AA.
AC Q75598;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein 120 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KI4803;
RX MEDLINE=96251941; PubMed=8661395; DOI=10.1006/viro.1996.0332;
RA McKeating J.A., Zhang Y.J., Arnold C., Frederiksson R., Fenyo E.M.,
RA Balfe P.;
RT "Chimeric viruses expressing primary envelope glycoproteins of human
RT immunodeficiency virus type I show increased sensitivity to
RT neutralization by human sera.";
RL Virology 220:450-460(1996).
DR EMBL; U57789; AAB17027.1; -.
DR HSSP; P04578; 1GCI.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
FT NON_TER 1
FT NON_TER 545
FT NON_TER 545
SQ SEQUENCE 545 AA; 60934 MW; 15CD203BB89DEADC CRC64;

Query Match 86.7%; Score 39; DB 2; Length 545;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 185 FVSLDIVPI 193

RESULT 12
Q6BC09
ID Q6BC09 PRELIMINARY; PRT; 843 AA.
AC Q6BC09;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)

25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Envelope glycoprotein (fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Binley J.M., Wrin T., Zwick M.B., Korber B., Wang M., Chappey C.,
 RA Stiegler G., Kunert R., Zolla-Pazner S., Katinger H.,
 RA Petropoulos C.J., Burton D.R.;
 RT "Comprehensive analysis of the cross-clade neutralizing activity of a
 RT panel of anti-Hiv-1 monoclonal antibodies.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY669733; AAT67505.1; -;
 DR GO; GO:0019031; C: integral to membrane; IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR InterPro; IPR011010; DNA brk join_enz.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 FT NON TER 843 843
 SQ SEQUENCE 843 AA; 95773 MW; 4790D380C312969D CRC64;

 Query Match 86.7%; Score 39; DB 2; Length 843;
 Best Local Similarity 88.9%; Pred. No. 29;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 FVSLKIVPI 9
 DB 168 FVSLDIVPI 176

 RESULT 13
 Q6XJ60 PRELIMINARY; PRT; 846 AA.
 AC Q6XJ60;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Envelope glycoprotein.
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Vachot L., Ataman-Onal Y., Terrat C., Durand P.-Y., Ponceau B.,
 RA Biron F., Verrier B.;
 RT "Retrospective Study to Time the Introduction of HIV Type 1 Non-B
 RT Subtypes in Lyon, France, Using env Genes Obtained from Primary
 RT Infection Samples.";
 RL AIDS Res. Hum. Retroviruses 20:687-691 (2004).
 DR EMBL; AY231157; AAO84281.1; -;
 DR HSSP; P04578; 1K33.
 DR GO; GO:0019031; C: viral envelope; IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000328; Env GP41.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR PRINTS; PR01415; ANKYRIN
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 SQ SEQUENCE 846 AA; 95186 MW; 726985C4A62FC942 CRC64;

 Query Match 86.7%; Score 39; DB 2; Length 846;
 Best Local Similarity 88.9%; Pred. No. 29;

 QY 1 FVSLKIVPI 9
 DB 168 FVSLDIVPI 176

 RESULT 14
 Q6HIQ0 PRELIMINARY; PRT; 851 AA.
 AC Q6HIQ0;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Env glycoprotein.
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Thomson M.M., Sierra M., Tanuri A., Najera R.;
 RT "Independent origins of human immunodeficiency virus type 1 BF
 RT intersubtype recombinant viruses from Brazil revealed by analysis of
 RT near full-length genome sequences.";
 RL AIDS Res. Hum. Retroviruses 0:0-0 (2004).
 DR EMBL; AY455782; AAS5219.1; -;
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0019028; C: viral capsid; IEA.
 DR GO; GO:0019031; C: viral envelope; IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 851 AA; 95766 MW; 92105D4C446660E4 CRC64;

 Query Match 86.7%; Score 39; DB 2; Length 851;
 Best Local Similarity 88.9%; Pred. No. 29;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 FVSLKIVPI 9
 DB 178 FVSLDIVPI 186

 RESULT 15
 Q92890 PRELIMINARY; PRT; 864 AA.
 AC Q92890;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein.
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Celrichs R.B., McPhee D.A., Deacon N.J.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF042102; AAD03215.1; -;
 DR HSSP; P04578; 1DLB.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0019028; C: viral capsid; IEA.
 DR GO; GO:0019031; C: viral envelope; IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.

KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide; Polypeptide;
KW Transmembrane.
SQ SEQUENCE 864 AA; 97872 MW; E0352117099885E5 CRC64;
Query Match 86.7%; Score 39; DB 2; Length 864;
Best Local Similarity 88.9%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 FVSLKIVPI 9
Db 182 FVSLDIVPI 190
RESULT 16
Q69722 PRELIMINARY; PRT; 37 AA.
AC Q69722;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein, vlv2 region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirus; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U09153; AAB53908.1;
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 37 37
SQ SEQUENCE 37 AA; 4276 MW; D7E9287BE6461B99 CRC64;
Query Match 84.4%; Score 38; DB 2; Length 37;
Best Local Similarity 77.8%; Pred. No. 2.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FVSLKIVPI 9
Db 20 FVSLDIVPI 28
RESULT 17
Q69724 PRELIMINARY; PRT; 48 AA.
AC Q69724;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein, vlv2 region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirus; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Slobod K.S., Rencher S.D., Farmer A., Smith F.S., Hurwitz J.L.;
RL "HIV type 1 envelope sequence diversity in inner city community.";
RT AIDS Res. Hum. Retroviruses 10:873-875(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U09153; AAB53908.1;
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 37 37
SQ SEQUENCE 37 AA; 4276 MW; D7E9287BE6461B99 CRC64;
Query Match 84.4%; Score 38; DB 2; Length 37;
Best Local Similarity 77.8%; Pred. No. 2.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FVSLKIVPI 9
Db 20 FVSLDIVPI 28
RESULT 17
Q69724 PRELIMINARY; PRT; 48 AA.
AC Q69724;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein, vlv2 region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirus; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Slobod K.S., Rencher S.D., Farmer A., Smith F.S., Hurwitz J.L.;
RL "HIV type 1 envelope sequence diversity in inner city community.";
RT AIDS Res. Hum. Retroviruses 10:873-875(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U09152; AAB53906.1;
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 52 52
SQ SEQUENCE 52 AA; 5882 MW; 1B12309C68752C73 CRC64;
Query Match 84.4%; Score 38; DB 2; Length 52;
Best Local Similarity 77.8%; Pred. No. 3.1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FVSLKIVPI 9
Db 30 FVSLDIVPI 38
RESULT 19
Q70903 PRELIMINARY; PRT; 91 AA.
ID Q70903
AC Q70903;
RT "HIV type 1 envelope sequence diversity in inner city community.";

RL AIDS Res. Hum. Retroviruses 10:873-875(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U09154; AAB53910.1;
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 48 48
SQ SEQUENCE 48 AA; 5535 MW; C9A5381C1523534C CRC64;
Query Match 84.4%; Score 38; DB 2; Length 48;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FVSLKIVPI 9
Db 28 FVSLDIVPI 36
RESULT 18
Q69720 PRELIMINARY; PRT; 52 AA.
AC Q69720;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein, vlv2 region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirus; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Slobod K.S., Rencher S.D., Farmer A., Smith F.S., Hurwitz J.L.;
RL "HIV type 1 envelope sequence diversity in inner city community.";
RT AIDS Res. Hum. Retroviruses 10:873-875(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U09152; AAB53906.1;
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 52 52
SQ SEQUENCE 52 AA; 5882 MW; 1B12309C68752C73 CRC64;
Query Match 84.4%; Score 38; DB 2; Length 52;
Best Local Similarity 77.8%; Pred. No. 3.1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 FVSLKIVPI 9
Db 30 FVSLDIVPI 38
RESULT 19
Q70903 PRELIMINARY; PRT; 91 AA.
ID Q70903
AC Q70903;
RT "HIV type 1 envelope sequence diversity in inner city community.";

DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein VIV2 region (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Corneliussen M., Goudsmit J.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA McEvilly M.M.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U13496; AAA73686.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000777; GP120.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 FT NON_TER 1 91
 FT NON_TER 91 91
 SQ SEQUENCE 91 AA; 10182 MW; 058E3B021F62D130 CRC64;
 Query Match 84.4%; Score 38; DB 2; Length 91;
 Best Local Similarity 77.8%; Pred. No. 5.3;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FVSLKIVPI 9
 Db 65 FVSLDVVFI 73
 RESULT 20
 QY99C16 PRELIMINARY; PRT; 92 AA.
 ID Q99C16;
 AC Q99C16;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Graton S., Cheynier R., Dumaurier M.J., Oksenhendler E.,
 RA Wain-Hobson S.;
 RT "Highly restricted spread of HIV-1 and multiply infected cells within
 RT splenic germinal centers.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14566-14571(2000).
 DR EMBL; AF319931; AAG52870.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000777; GP120.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 FT NON_TER 1 92
 FT NON_TER 92 92
 SQ SEQUENCE 92 AA; 10298 MW; 613F1B4D120DBE29 CRC64;
 Query Match 84.4%; Score 38; DB 2; Length 92;
 Best Local Similarity 77.8%; Pred. No. 5.4;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
 Db 58 FVSLDVVFI 66
 RESULT 21
 QY1257 PRELIMINARY; PRT; 92 AA.
 ID Q71257;
 AC Q71257;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein gp120 (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=95191064; PubMed=7884929;
 RA Wang N., Zhu T., Ho D.D.;
 RT "Sequence diversity of V1 and V2 domains of gp120 from human
 RT immunodeficiency virus type 1: lack of correlation with viral
 RT phenotype.";
 RL J. Virol. 69:2708-2715(1995).
 DR EMBL; U19627; AAA68644.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 FT NON_TER 1 92
 FT NON_TER 92 92
 SQ SEQUENCE 92 AA; 10269 MW; CB58433715CAA880 CRC64;
 Query Match 84.4%; Score 38; DB 2; Length 92;
 Best Local Similarity 77.8%; Pred. No. 5.4;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FVSLKIVPI 9
 Db 43 FVSLDVVFI 51
 RESULT 22
 QY1270 PRELIMINARY; PRT; 110 AA.
 ID Q71270;
 AC Q71270;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein gp120 (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=95191064; PubMed=7884929;
 RA Wang N., Zhu T., Ho D.D.;
 RT "Sequence diversity of V1 and V2 domains of gp120 from human
 RT immunodeficiency virus type 1: lack of correlation with viral
 RT phenotype.";
 RL J. Virol. 69:2708-2715(1995).
 DR EMBL; U19640; AAA68657.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.

```
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 110
SQ SEQUENCE 110 AA; 12466 MW; 35D3578DA359196 CRC64;

Query Match      84.4%; Score 38; DB 2; Length 110;
Best Local Similarity 77.8%; Pred. No. 6.4;
Matches 7; Conservative 1; Mismatches 0; Gaps 0; Indels 0;

QY 1 FVSLKIVPI 9
Db 62 FVSLDVVPI 70

RESULT 23
Q8JECO PRELIMINARY; PRT; 215 AA.
AC Q8JECO;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-JUN-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeuchi H., Suzuki Y., Hoshino H., Daar E.S., Koyanagi Y.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086285; C:integral to membrane; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 215
SQ SEQUENCE 215 AA; 23687 MW; E08C4B05E07147C8 CRC64;

Query Match      84.4%; Score 38; DB 2; Length 215;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 59 FVSLDVVPI 67

RESULT 24
Q8Q820 PRELIMINARY; PRT; 215 AA.
AC Q8Q820;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB077794; BAB5727.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.

KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 110
SQ SEQUENCE 110 AA; 12466 MW; 35D3578DA359196 CRC64;

Query Match      84.4%; Score 38; DB 2; Length 110;
Best Local Similarity 77.8%; Pred. No. 6.4;
Matches 7; Conservative 1; Mismatches 0; Gaps 0; Indels 0;

QY 1 FVSLKIVPI 9
Db 62 FVSLDVVPI 70

RESULT 23
Q8JECO PRELIMINARY; PRT; 215 AA.
AC Q8JECO;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-JUN-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeuchi H., Suzuki Y., Hoshino H., Daar E.S., Koyanagi Y.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086285; BAB02647.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 215
SQ SEQUENCE 215 AA; 23687 MW; E08C4B05E07147C8 CRC64;

Query Match      84.4%; Score 38; DB 2; Length 215;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 59 FVSLDVVPI 67

RESULT 24
Q8Q820 PRELIMINARY; PRT; 215 AA.
AC Q8Q820;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB077794; BAB5727.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
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DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 215
SQ SEQUENCE 215 AA; 23687 MW; E08C4B05E07147C8 CRC64;

Query Match      84.4%; Score 38; DB 2; Length 215;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 59 FVSLDVVPI 67

RESULT 25
Q8Q813 PRELIMINARY; PRT; 226 AA.
AC Q8Q813;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB077801; BAB85734.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 226
SQ SEQUENCE 226 AA; 25003 MW; 5816FDCFD520D6DA CRC64;

Query Match      84.4%; Score 38; DB 2; Length 226;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FVSLKIVPI 9
Db 61 FVSLDVVPI 69

RESULT 26
Q8Q814 PRELIMINARY; PRT; 230 AA.
AC Q8Q814;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB077800; BAB85733.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
```

DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 230 230
SQ SEQUENCE 230 AA; 25484 MW; 181C323B143A22D3 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 230;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
||||| :|||
Db 74 FYSLDVVPI 82

RESULT 27

ID Q8Q831 PRELIMINARY; PRT; 232 AA.
AC Q8Q831;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB077782; BAB85716.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 232 232
FT NON_TER 1
SQ SEQUENCE 232 AA; 25529 MW; CC6AD5DD7964104B CRC64;

Query Match 84.4%; Score 38; DB 2; Length 232;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
||||| :|||
Db 76 FYSLDVVPI 84

RESULT 28

ID Q8JE87 PRELIMINARY; PRT; 233 AA.
AC Q8JE87;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeuchi H., Suzuki Y., Hoshino H., Daar E.S., Koyanagi Y.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086318; BAC02680.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 233 233
SQ SEQUENCE 233 AA; 25810 MW; F101792FD2515941 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 233;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
||||| :|||
Db 61 FYSLDVVPI 69

RESULT 29

ID Q8JE88 PRELIMINARY; PRT; 233 AA.
AC Q8JE88;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeuchi H., Suzuki Y., Hoshino H., Daar E.S., Koyanagi Y.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086317; BAC02679.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000985; ConA_like_lec_gl.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 233 233
FT NON_TER 1
SQ SEQUENCE 233 AA; 25680 MW; E07FDEF7B83C3A21 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 233;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
||||| :|||
Db 76 FYSLDVVPI 84

RESULT 30

ID Q8Q816 PRELIMINARY; PRT; 233 AA.
AC Q8Q816;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB077798; BAB85731.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.

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DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 233
SQ SEQUENCE 233 AA; 25810 MW; F101792FD2515941 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 233;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FVSLKIVPI 9
    ||||:||||
Db 61 FVSLDVVPI 69

RESULT 31
Q8Q819 PRELIMINARY; PRT; 233 AA.
AC Q8Q819;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB077795; BAB85728.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 233
SQ SEQUENCE 233 AA; 25680 MW; E07FDEF7B83C3A21 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 233;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FVSLKIVPI 9
    ||||:||||
Db 76 FVSLDVVPI 84

RESULT 32
Q8Q812 PRELIMINARY; PRT; 234 AA.
AC Q8Q812;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
```

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DR EMBL; AB077802; BAB85735.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 234
SQ SEQUENCE 234 AA; 25944 MW; 096B484F44880D8D CRC64;

Query Match 84.4%; Score 38; DB 2; Length 234;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FVSLKIVPI 9
    ||||:||||
Db 61 FVSLDVVPI 69

RESULT 33
Q8JE89 PRELIMINARY; PRT; 242 AA.
AC Q8JE89;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeuchi H., Suzuki Y., Hoshino H., Daar E.S., Koyanagi Y.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086316; BAC02678.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 242
SQ SEQUENCE 242 AA; 26715 MW; 1C0C2D1685D5380 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 242;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FVSLKIVPI 9
    ||||:||||
Db 86 FVSLDVVPI 94

RESULT 34
Q8Q832 PRELIMINARY; PRT; 242 AA.
AC Q8Q832;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;
```

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB077781; BAB85715.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0019028; C: viral capsid; IEA.
 DR GO; GO:0019031; C: viral envelope; IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 FT NON_TER 242 242
 FT NON_TER 242 242
 SQ SEQUENCE 242 AA; 26715 MW; 1C0C2D16855D5380 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 242;
 Best Local Similarity 77.8%; Pred. No. 14;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
 |||| :|||
 Db 86 FYSLDVVPI 94

RESULT 35

Q8Q836 PRELIMINARY; PRT; 242 AA.
 ID Q8Q836
 AC Q8Q836
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB077777; BAB85711.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0019028; C: viral capsid; IEA.
 DR GO; GO:0019031; C: viral envelope; IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 FT NON_TER 242 242
 FT NON_TER 242 242
 SQ SEQUENCE 242 AA; 26613 MW; 4D616E967D6786CD CRC64;

Query Match 84.4%; Score 38; DB 2; Length 242;
 Best Local Similarity 77.8%; Pred. No. 14;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
 |||| :|||
 Db 86 FYSLDVVPI 94

RESULT 36

P88361 PRELIMINARY; PRT; 244 AA.
 ID P88361
 AC P88361
 DT 01-MAY-1997 (TRENBLrel. 03, Created)
 DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.

RA MEDLINE=97184515; PubMed=9032317;
 RA McDonald R.A., Mayers D.L., Chung R.C., Wagner K.F., Ratto-Kim S.,
 RA Bix D.L., Michael N.L.;
 RT "Evolution of human immunodeficiency virus type 1 env sequence
 RT variation in patients with diverse rates of disease progression and T-
 RT cell function.";
 RL J. Virol. 71:1871-1879(1997).
 DR EMBL; U69437; AAC56748.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0019028; C: viral capsid; IEA.
 DR GO; GO:0019031; C: viral envelope; IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 FT NON_TER 244 244
 FT NON_TER 244 244
 SQ SEQUENCE 244 AA; 27027 MW; 37164D083DDAC3D1 CRC64;

Query Match 84.4%; Score 38; DB 2; Length 244;
 Best Local Similarity 77.8%; Pred. No. 14;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
 |||| :|||
 Db 58 FYSLDVVPI 66

RESULT 37

Q8Q818 PRELIMINARY; PRT; 244 AA.
 ID Q8Q818
 AC Q8Q818
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB077796; BAB85729.1; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0019028; C: viral capsid; IEA.
 DR GO; GO:0019031; C: viral envelope; IEA.
 DR GO; GO:0005198; F: structural molecule activity; IEA.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 FT NON_TER 244 244
 FT NON_TER 244 244
 SQ SEQUENCE 244 AA; 27115 MW; 6855D05984F1EBDA CRC64;

Query Match 84.4%; Score 38; DB 2; Length 244;
 Best Local Similarity 77.8%; Pred. No. 14;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
 |||| :|||
 Db 61 FYSLDVVPI 69

RESULT 38

Q8Q815 PRELIMINARY; PRT; 245 AA.
 ID Q8Q815
 AC Q8Q815
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).

```
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB077799; BAB85732.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 245
SQ SEQUENCE 245 AA; 27285 MW; 6B11726B82AA3EE5 CRC64;

Query Match      84.4%; Score 38; DB 2; Length 245;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
Db 64 FYSLDVVP 72

RESULT 39
Q80827 PRELIMINARY; PRT; 248 AA.
AC Q80827;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeuchi H., Suzuki Y., Daar E.S., Koyanagi Y.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB077786; BAB85720.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 248
SQ SEQUENCE 248 AA; 27443 MW; 98CB3F4051C823D4 CRC64;

Query Match      84.4%; Score 38; DB 2; Length 248;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
Db 85 FYSLDVVP 93

RESULT 40
P88346 PRELIMINARY; PRT; 249 AA.
AC P88346;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
```

```
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA McDonald R.A., Mayers D.L., Chung R.C., Wagner K.F., Ratto-Kim S.,
RA Bix D.L., Michael N.L.;
RL "Evolution of human immunodeficiency virus type 1 env sequence
RT variation in patients with diverse rates of disease progression and T-
RT cell function.";
RL J. Virol. 71:1871-1879(1997).
DR EMBL; U69422; AAC56733.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 249
SQ SEQUENCE 249 AA; 27639 MW; B3975A61EE9E2DD0 CRC64;

Query Match      84.4%; Score 38; DB 2; Length 249;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FYSLKIVPI 9
Db 62 FYSLDVVP 70
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Search completed: February 24, 2005, 19:14:38
Job time : 176 secs